

Sequence Comparison
US-09-876-790-1.rni

```
QY 484 GGGGTGACAGATAATTTGAGAACGAAACATTTGATTTTCAATTCACACGTTTGC 543
D 619 GGGGTGACAGATAATTTGAGAACGAAACATTTGATTTTCAATTCACACGTTTGC 678
QY 544 AAAGCTAAATGAGCCCGAGTGGAGTGGAGGATTAG 579
D 679 AAAGCTAAATGAGCCCGAGTGGAGTGGAGGATTAG 714
```

RESULT 2
US-09-128-155-1

```
Sequence 1, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 989
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (356)...(889)
US-09-128-155-1
```

Query Match Best Local Similarity 68.3%; Score 395.2; DB 3; Length 989;
Matches 400; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```
QY 172 AACTACATACGCCAGAGATCTTTGCAATAGCCTCATCTTGAGCTCAGCTCGG 231
D 485 AATTTGTTCAACAAAGATCTTTGCAATAGCCTCATCTTGAGCTCAGCTCGG 544
QY 232 GAGAAAGAGTCCGATCTCTGGGGGTCTTAAAGGGAGTTTGTCTACTGTAC 291
D 545 GAGAAAGAGTCCGATCTCTGGGGGTCTTAAAGGGAGTTTGTCTACTGTAC 604
QY 292 AAGATTAAGGACAAAGATCATCCCTCAGCTGAAGAGAGAACTGATGAGCTG 351
D 605 AAGATTAAGGACAAAGATCATCCCTCAGCTGAAGAGAGAACTGATGAGCTG 664
QY 352 GCTGCCCAAAAGAGATCAGACGCCGGCCCTTCATCTTTATAGGGCTCAGTGGGCTCC 411
D 665 GCTGCCCAAAAGAGATCAGACGCCGGCCCTTCATCTTTATAGGGCTCAGTGGGCTCC 724
QY 412 TGAACATGCTGAGTGGGGGTCCACCCGGATGCTTATCTGACCTCTGCAATTGT 471
D 725 TGAACATGCTGAGTGGGGGTCCACCCGGATGCTTATCTGACCTCTGCAATTGT 784
QY 472 AATGAGCTTTGGGGTGAAGATAATTTGAGAACGAAACATTTGATTTTCAATTT 531
D 785 AATGAGCTTTGGGGTGAAGATAATTTGAGAACGAAACATTTGATTTTCAATTT 844
QY 532 CAACCAAGTTGCAAGCTGAAGTGAAGCCCGAGTGGAGTCAAGCATTAG 579
D 845 CAACCAAGTTGCAAGCTGAAGTGAAGCCCGAGTGGAGTCAAGCATTAG 892
```

RESULT 3
US-09-128-155-10
Sequence 10, Application US/09128155
Patent No. 6117654

```
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 408
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(408)
US-09-128-155-10
```

Query Match Best Local Similarity 67.7%; Score 392.2; DB 3; Length 408;
Matches 397; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```
QY 172 AACTACATACGCCAGAGATCTTTGCAATAGCCTCATCTTGAGCTCAGCTCGG 231
D 4 AATTTGTTCAACAAAGATCTTTGCAATAGCCTCATCTTGAGCTCAGCTCGG 63
QY 232 GAGAAAGAGTCCGATCTCTGGGGGTCTTAAAGGGAGTTTGTCTACTGTAC 291
D 64 GAGAAAGAGTCCGATCTCTGGGGGTCTTAAAGGGAGTTTGTCTACTGTAC 123
QY 292 AAGATTAAGGACAAAGATCATCCCTCAGCTGAAGAGAGAACTGATGAGCTG 351
D 124 AAGATTAAGGACAAAGATCATCCCTCAGCTGAAGAGAGAACTGATGAGCTG 183
QY 352 GCTGCCCAAAAGAGATCAGACGCCGGCCCTTCATCTTTATAGGGCTCAGTGGGCTCC 411
D 184 GCTGCCCAAAAGAGATCAGACGCCGGCCCTTCATCTTTATAGGGCTCAGTGGGCTCC 243
QY 412 TGAACATGCTGAGTGGGGGTCCACCCGGATGCTTATCTGACCTCTGCAATTGT 471
D 244 TGAACATGCTGAGTGGGGGTCCACCCGGATGCTTATCTGACCTCTGCAATTGT 303
QY 472 AATGAGCTTTGGGGTGAAGATAATTTGAGAACGAAACATTTGATTTTCAATTT 531
D 304 AATGAGCTTTGGGGTGAAGATAATTTGAGAACGAAACATTTGATTTTCAATTT 363
QY 532 CAACCAAGTTGCAAGCTGAAGTGAAGCCCGAGTGGAGTCAAGCATTAG 576
D 364 CAACCAAGTTGCAAGCTGAAGTGAAGCCCGAGTGGAGTCAAGCATTAG 408
```

RESULT 4
US-09-128-155-6
Sequence 6, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6

GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2003, 18:32:50 ; Search time 64 Seconds

(without alignments)
88.269 Million cell updates/sec

Title: US-09-876-790-3

Perfect score: 1017

Sequence: 1 MSGCDRETTETKGNSEFKR.....IEFSFPYCKAEMSPSEVSD 192

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA.*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*

2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*

3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*

4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*

5: /cgn2_6/ptodata/1/1aa/PCFUS.COMB.pep.*

6: /cgn2_6/ptodata/1/1aa/Backfilltest.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	895	88.0	218	4	US-09-293-625-2
2	702	69.0	167	3	US-09-128-155-7
3	702	69.0	178	3	US-09-128-155-2
4	695	68.3	136	3	US-09-128-155-11
5	623	61.3	115	3	US-09-128-155-5
6	623	61.3	115	3	US-09-128-155-9
7	623	61.3	115	3	US-09-128-155-13
8	473.5	46.6	185	3	US-09-128-155-18
9	225.5	22.2	169	2	US-08-790-032-2
10	225.5	22.2	169	3	US-09-069-619-2
11	225.5	22.2	169	4	US-09-494-018-2
12	172.5	17.0	155	4	US-09-417-455-5
13	172.5	17.0	155	4	US-09-348-942-5
14	172.5	17.0	155	4	US-09-316-081-5
15	172.5	17.0	155	4	US-09-578-458-5
16	172.5	17.0	155	4	US-09-522-964A-5
17	172.5	17.0	155	4	US-09-457-626-5
18	165.5	16.3	152	4	US-09-578-458-18
19	159	15.6	178	3	US-09-000-630C-21
20	159	15.6	178	3	US-08-862-730C-21
21	159	15.6	178	4	US-09-417-455-9
22	159	15.6	178	4	US-09-348-942-9
23	155.5	15.3	178	4	US-09-457-626-9
24	155.5	15.3	152	4	US-09-316-081-2
25	155.5	15.3	152	4	US-09-578-458-2
26	155.5	15.3	152	4	US-09-522-964A-2
27	155.5	15.3	153	3	US-08-677-778B-1

28	155.5	15.3	169	4	US-09-316-081-4	Sequence 4, Appl
29	155.5	15.3	169	4	US-09-578-458-4	Sequence 4, Appl
30	155.5	15.3	169	4	US-09-522-964A-4	Sequence 4, Appl
31	155.5	15.3	200	4	US-09-578-458-13	Sequence 13, Appl
32	155.5	15.3	200	4	US-09-522-964A-13	Sequence 13, Appl
33	151.5	14.9	177	3	US-09-000-630C-22	Sequence 22, Appl
34	151.5	14.9	177	3	US-08-862-730C-22	Sequence 22, Appl
35	151.5	14.9	177	4	US-09-417-455-11	Sequence 11, Appl
36	151.5	14.9	177	4	US-09-348-942-11	Sequence 11, Appl
37	151.5	14.9	177	4	US-09-457-626-11	Sequence 11, Appl
38	150.5	14.8	180	1	US-08-476-860-13	Sequence 13, Appl
39	150.5	14.8	180	2	US-08-910-733-13	Sequence 13, Appl
40	150.5	14.8	180	2	US-08-910-884-13	Sequence 13, Appl
41	150.5	14.8	389	4	US-09-131-247-14	Sequence 14, Appl
42	149.5	14.7	153	3	US-08-798-414-2	Sequence 2, Appl
43	149.5	14.7	153	4	US-09-131-247-2	Sequence 2, Appl
44	149.5	14.7	153	4	US-09-131-247-4	Sequence 4, Appl
45	149.5	14.7	156	1	US-08-476-860-10	Sequence 10, Appl

ALIGNMENTS

```
RESULT 1
US-09-293-625-2
; Sequence 2, Application US/09293625
; Patent No. 6342371
; GENERAL INFORMATION:
; APPLICANT: Young, Peter R.
; APPLICANT: McDonnell, Peter C
; TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, IL-1H4
; FILE REFERENCE: GP-70607
; CURRENT APPLICATION NUMBER: US/09/293,625
; CURRENT FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-293-625-2

Query Match      88.0%; Score 895; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 4.3e-98;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 PKYKNLMPKFFSIHDDHKVLYLDSGNLAVPPKNYIRPIFFALASSSASAEKGSPT 83
    |||
DB 50 PKYKNLMPKFFSIHDDHKVLYLDSGNLAVPPKNYIRPIFFALASSSASAEKGSPT 109
    |||
QY 84 LLGYSKEFFCYCDKDGSHPSIOLKKEKMLAOKESARPPFYRQVGSMMLES 143
    |||
DB 110 LLGYSKEFFCYCDKDGSHPSIOLKKEKMLAOKESARPPFYRQVGSMMLES 169
    |||
QY 144 AAHPGWFICTSCNCEPVGVTDFENRKHIEFSFPYCKAEMSPSEVSD 192
    |||
DB 170 AAHPGWFICTSCNCEPVGVTDFENRKHIEFSFPYCKAEMSPSEVSD 218
    |||

RESULT 2
US-09-128-155-7
; Sequence 7, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
```

Sequence Comparison
B

see over

Sequence
Comparison
B

```
;; EARLIER FILING DATE: 1997-08-04
;; NUMBER OF SEQ ID NOS: 18
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 7
;; LENGTH: 167
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-128-155-7
```

Query Match 69.0%; Score 702; DB 3; Length 167;
Best Local Similarity 93.6%; Pred. No. 2.3e-75;
Matches 131; Conservative 5; Mismatches 4; Indels 0; Gaps 0

```
QY 53 AVPDKNYIRPEIFALASSLSASAEKSPILLGVSGEFLCYCDKDGQSHPSLQKKE 112
Db 28 SLEPTMFEVHTKIFALASSLSASAEKSPILLGVSGEFLCYCDKDGQSHPSLQKKE 87
QY 113 KLMLIAOKESARRPFIFYRAQVGSWMNLESAAHPGMFICTSCNCPNEPVGTDKFEENRKH 172
Db 88 KLMLIAOKESARRPFIFYRAQVGSWMNLESAAHPGMFICTSCNCPNEPVGTDKFEENRKH 147
QY 173 IEFSPQVCKAEMSPSEVSD 192
Db 148 IEFSPQVCKAEMSPSEVSD 167
```

RESULT 3
US-09-128-155-2
Sequence 2, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/052001
CURRENT FILING DATE: US/09/128.155
EARLIER FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091.650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054.646
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 178
TYPE: PRT
ORGANISM: Homo sapiens
US-09-128-155-2

```
QY 53 AVPDKNYIRPEIFALASSLSASAEKSPILLGVSGEFLCYCDKDGQSHPSLQKKE 112
Db 39 SLEPTMFEVHTKIFALASSLSASAEKSPILLGVSGEFLCYCDKDGQSHPSLQKKE 98
QY 113 KLMLIAOKESARRPFIFYRAQVGSWMNLESAAHPGMFICTSCNCPNEPVGTDKFEENRKH 172
Db 99 KLMLIAOKESARRPFIFYRAQVGSWMNLESAAHPGMFICTSCNCPNEPVGTDKFEENRKH 158
QY 173 IEFSPQVCKAEMSPSEVSD 192
Db 159 IEFSPQVCKAEMSPSEVSD 178
```

RESULT 4
US-09-128-155-11
Sequence 11, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY

```
;; TITLE OF INVENTION: AND USES THEREOF
;; FILE REFERENCE: 09404/052001
;; CURRENT APPLICATION NUMBER: US/09/128.155
;; CURRENT FILING DATE: 1998-08-03
;; EARLIER APPLICATION NUMBER: US 60/091.650
;; EARLIER FILING DATE: 1998-07-02
;; EARLIER APPLICATION NUMBER: US 60/054.646
;; EARLIER FILING DATE: 1997-08-04
;; NUMBER OF SEQ ID NOS: 18
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 11
;; LENGTH: 136
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-128-155-11
```

Query Match 68.3%; Score 695; DB 3; Length 136;
Best Local Similarity 96.3%; Pred. No. 1.1e-74;
Matches 130; Conservative 3; Mismatches 2; Indels 0; Gaps 0

```
QY 58 NYRPEIFALASSLSASAEKSPILLGVSGEFLCYCDKDGQSHPSLQKKEKIMKL 117
Db 2 NFVHTKIFALASSLSASAEKSPILLGVSGEFLCYCDKDGQSHPSLQKKEKIMKL 61
QY 118 AAKESARRPFIFYRAQVGSWMNLESAAHPGMFICTSCNCPNEPVGTDKFEENRKHIEFSF 177
Db 62 AAKESARRPFIFYRAQVGSWMNLESAAHPGMFICTSCNCPNEPVGTDKFEENRKHIEFSF 121
QY 178 QPVCKAEMSPSEVSD 192
Db 122 QPVCKAEMSPSEVSD 136
```

RESULT 5
US-09-128-155-5
Sequence 5, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128.155
CURRENT FILING DATE: 1998-08-03
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/091.650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054.646
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 115
TYPE: PRT
ORGANISM: Homo sapiens
US-09-128-155-5

Query Match 61.3%; Score 623; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 3.1e-66;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 78 EKSPILLGVSGEFLCYCDKDGQSHPSLQKKEKIMLAOKESARRPFIFYRAQVGS 137
Db 1 EKSPILLGVSGEFLCYCDKDGQSHPSLQKKEKIMLAOKESARRPFIFYRAQVGS 60
QY 138 WMNLESAAHPGMFICTSCNCPNEPVGTDKFEENRKHIEFSFQPVCKAEMSPSEVSD 192
Db 61 WMNLESAAHPGMFICTSCNCPNEPVGTDKFEENRKHIEFSFQPVCKAEMSPSEVSD 115
```

RESULT 6
US-09-128-155-9
Sequence 9, Application US/09128155
Patent No. 6117654

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2003, 18:32:50 : Search time 64 Seconds
(without alignments)
88.269 Million cell updates/sec

Title: US-09-876-790-3
Perfect score: 1017
Sequence: 1 MSGCDRETETKGNKSFKKR.....IEFSFQVCKAEMSPSEVSD 192

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	895	88.0	218	4	US-09-293-625-2
2	702	69.0	167	3	US-09-128-155-7
3	702	69.0	178	3	US-09-128-155-7
4	695	68.3	136	3	US-09-128-155-11
5	623	61.3	115	3	US-09-128-155-5
6	623	61.3	115	3	US-09-128-155-9
7	623	61.3	115	3	US-09-128-155-13
8	473.5	46.6	185	3	US-09-128-155-18
9	225.5	22.2	169	2	US-08-790-032-2
10	225.5	22.2	169	3	US-09-069-619-2
11	225.5	22.2	169	4	US-09-494-018-2
12	172.5	17.0	155	4	US-09-417-455-5
13	172.5	17.0	155	4	US-09-348-842-5
14	172.5	17.0	155	4	US-09-316-081-5
15	172.5	17.0	155	4	US-09-578-458-5
16	172.5	17.0	155	4	US-09-522-964A-5
17	172.5	17.0	155	4	US-09-457-626-5
18	165.5	16.3	152	4	US-09-578-458-18
19	159	15.6	178	3	US-09-000-630C-21
20	159	15.6	178	3	US-08-862-730C-21
21	159	15.6	178	4	US-09-417-455-9
22	159	15.6	178	4	US-09-348-942-9
23	159	15.6	178	4	US-09-457-626-9
24	155.5	15.3	152	4	US-09-316-081-2
25	155.5	15.3	152	4	US-09-578-458-2
26	155.5	15.3	152	4	US-09-522-964A-2
27	155.5	15.3	153	3	US-08-677-778B-1

28	155.5	15.3	169	4	US-09-316-081-4	Sequence 4, Appl1
29	155.5	15.3	169	4	US-09-578-458-4	Sequence 4, Appl1
30	155.5	15.3	169	4	US-09-522-964A-4	Sequence 4, Appl1
31	155.5	15.3	200	4	US-09-578-458-13	Sequence 13, Appl1
32	155.5	15.3	200	4	US-09-522-964A-13	Sequence 13, Appl1
33	151.5	14.9	177	3	US-09-000-630C-22	Sequence 22, Appl1
34	151.5	14.9	177	3	US-08-862-730C-22	Sequence 22, Appl1
35	151.5	14.9	177	4	US-09-417-455-11	Sequence 11, Appl1
36	151.5	14.9	177	4	US-09-348-942-11	Sequence 11, Appl1
37	151.5	14.9	177	4	US-09-457-626-11	Sequence 11, Appl1
38	150.5	14.8	180	1	US-08-476-860-13	Sequence 13, Appl1
39	150.5	14.8	180	2	US-08-910-733-13	Sequence 13, Appl1
40	150.5	14.8	180	2	US-08-910-884-13	Sequence 13, Appl1
41	150.5	14.8	389	4	US-09-131-247-14	Sequence 14, Appl1
42	149.5	14.7	153	3	US-08-798-414-2	Sequence 2, Appl1
43	149.5	14.7	153	4	US-09-131-247-2	Sequence 2, Appl1
44	149.5	14.7	153	4	US-09-131-247-4	Sequence 4, Appl1
45	149.5	14.7	156	1	US-08-476-860-10	Sequence 10, Appl1

ALIGNMENTS

```
RESULT 1
US-09-293-625-2
; Sequence 2, Application US/09293625
; Patent No. 6342371
; GENERAL INFORMATION:
; APPLICANT: Young, Peter R.
; APPLICANT: McDonnell, Peter C
; TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, IL-1H4
; FILE REFERENCE: GP-70607
; CURRENT APPLICATION NUMBER: US/09/293,625
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-293-625-2

Query Match      88.0%; Score 895; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 4.3e-98;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 PKYKNINPKKFSIHDDHVLVDLSNLAIVDDKNTYRPIFFALASSISASAKGSP1 83
DB 50 PKYKNINPKKFSIHDDHVLVDLSNLAIVDDKNTYRPIFFALASSISASAKGSP1 109
QY 84 ILGVSQGECLYCDKDKGSHPSLQLEKELKLAOKESARRPFTFYAOGVSNMMLES 143
DB 110 ILGVSQGECLYCDKDKGSHPSLQLEKELKLAOKESARRPFTFYAOGVSNMMLES 169
QY 144 AAHPGWFICTSCNCPVGTDTKFEENRKHIIEFSFQVCKAEMSPSEVSD 192
DB 170 AAHPGWFICTSCNCPVGTDTKFEENRKHIIEFSFQVCKAEMSPSEVSD 218

RESULT 2
US-09-128-155-7
; Sequence 7, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
```

```
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-7

Query Match
Best Local Similarity 93.6%; Score 702; DB 3; Length 167;
Matches 131; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 53 AVPDKNYIRPEIFALASSLSASAEKSGPILLGVSKGEFCLYCDKDGQSHPSLQKKE 112
    ::::: :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 28 SLPTNMFVHTKIFALASSLSASAEKSGPILLGVSKGEFCLYCDKDGQSHPSLQKKE 87
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
OY 113 KLMTAAOKESARRPFIYRAQVGSNMNLSAAHPGWFICTSCNCPYGVTDKFNKRKH 172
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 88 KLMTAAOKESARRPFIYRAQVGSNMNLSAAHPGWFICTSCNCPYGVTDKFNKRKH 147
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
OY 173 IEFSPQVCKAEMSPSEVSD 192
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 148 IEFSPQVCKAEMSPSEVSD 167

RESULT 3
US-09-128-155-2
; Sequence 2, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-2

Query Match
Best Local Similarity 93.6%; Score 702; DB 3; Length 178;
Matches 131; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 53 AVPDKNYIRPEIFALASSLSASAEKSGPILLGVSKGEFCLYCDKDGQSHPSLQKKE 112
    ::::: :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 39 SLPTNMFVHTKIFALASSLSASAEKSGPILLGVSKGEFCLYCDKDGQSHPSLQKKE 98
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
OY 113 KLMTAAOKESARRPFIYRAQVGSNMNLSAAHPGWFICTSCNCPYGVTDKFNKRKH 172
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 99 KLMTAAOKESARRPFIYRAQVGSNMNLSAAHPGWFICTSCNCPYGVTDKFNKRKH 158
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
OY 173 IEFSPQVCKAEMSPSEVSD 192
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 159 IEFSPQVCKAEMSPSEVSD 178

RESULT 4
US-09-128-155-11
; Sequence 11, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
```

```
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-11

Query Match
Best Local Similarity 96.3%; Score 695; DB 3; Length 136;
Matches 130; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 58 NYIRPEIFALASSLSASAEKSGPILLGVSKGEFCLYCDKDGQSHPSLQKKEKML 117
    ::::: :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 2 NFVHTKIFALASSLSASAEKSGPILLGVSKGEFCLYCDKDGQSHPSLQKKEKML 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
OY 118 AAKESARRPFIYRAQVGSNMNLSAAHPGWFICTSCNCPYGVTDKFNKRKHIEFSF 177
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 62 AAKESARRPFIYRAQVGSNMNLSAAHPGWFICTSCNCPYGVTDKFNKRKHIEFSF 121
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
OY 178 QPVCKAEMSPSEVSD 192
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 122 QPVCKAEMSPSEVSD 136

RESULT 5
US-09-128-155-5
; Sequence 5, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-5

Query Match
Best Local Similarity 100.0%; Score 623; DB 3; Length 115;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 EKSGPILLGVSKGEFCLYCDKDGQSHPSLQKKEKLMTAAOKESARRPFIYRAQVGS 137
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 EKSGPILLGVSKGEFCLYCDKDGQSHPSLQKKEKLMTAAOKESARRPFIYRAQVGS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
OY 138 WNMLESAAHPGWFICTSCNCPYGVTDKFNKRKHIEFSROPVCKAEMSPSEVSD 192
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 WNMLESAAHPGWFICTSCNCPYGVTDKFNKRKHIEFSROPVCKAEMSPSEVSD 115

RESULT 6
US-09-128-155-9
; Sequence 9, Application US/09128155
; Patent No. 6117654
```

```

: GENERAL INFORMATION:
: APPLICANT: Pan, Yang
: TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
: TITLE OF INVENTION: AND USES THEREOF
: FILE REFERENCE: 09404/052001
: CURRENT APPLICATION NUMBER: US/09/128,155
: CURRENT FILING DATE: 1998-08-03
: EARLIER APPLICATION NUMBER: US 60/091,650
: EARLIER FILING DATE: 1998-07-02
: EARLIER APPLICATION NUMBER: US 60/054,646
: EARLIER FILING DATE: 1997-08-04
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 9
: LENGTH: 115
: TYPE: PRT
: ORGANISM: Homo sapiens
: OS-09-128-155-9

```

Query Match	11.3%	Score 623;	DB 3;	Length 115;
Best Local Similarity	100.0%;	Pred. No. 3,	le-66;	
Matches 115;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps
QY	78	EKSGPILLGVSKGEPCLYCDPKDKQSHPSLTQKKEKMTLAAQKESARRPFIIFYRAQVGS	137	
Db	1	EKSGPILLGVSKGEPCLYCDPKDKQSHPSLTQKKEKMTLAAQKESARRPFIIFYRAQVGS	60	
QY	138	WNMLESAHPGWFICTSCNCENPVGYTDKEFNKRHHIEFSPQVYCAKEMSPSEVSD	192	
Db	61	WNMLESAHPGWFICTSCNCENPVGYTDKEFNKRHHIEFSPQVYCAKEMSPSEVSD	115	

```

RESULT 7
US-09-128-155-13
; Sequence 13, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ. ID NOS: 18
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 115
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-128-155-13

```

Query Match	61.3%	Score	623	DB 3:	Length	115:
Best Local Similarity	100.0%	Pred. No.	3,1e-66:			
Matches	115:	Conservative	0:	Mismatches	0:	Gaps
QY	78	EGSGPLLGVSGEGECILCDKDRKGSHSLQKKEKMLKLAQKESARRPIIFYRAVGS	137			
DB	1	EGSGPLLGVSGEGECILCDKDRKGSHSLQKKEKMLKLAQKESARRPIIFYRAVGS	60			
QY	138	WNLESAAPAHGAFICTSCNENPEVAVTDKFNKRKHIEFSFQVPCAKESPSVEVD	192			
DB	61	WNLESAAPAHGAFICTSCNENPEVAVTDKFNKRKHIEFSFQVPCAKESPSVEVD	115			

RESULT 8
US-09-128-155-18
; Sequence 18, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:

```

1  APPLICANT: Pan, Yang
2  TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
3  TITLE OF INVENTION: AND USES THEREOF
4  FILE REFERENCE: 09404/052001
5  CURRENT APPLICATION NUMBER: US/09/128,155
6  CURRENT FILING DATE: 1998-08-03
7  EARLIER APPLICATION NUMBER: US 60/091,650
8  EARLIER FILING DATE: 1998-07-02
9  EARLIER APPLICATION NUMBER: US 60/054,646
10 EARLIER FILING DATE: 1997-08-04
11 NUMBER OF SEQ ID NOS: 18
12 SOFTWARE: FastSeq for Windows Version 3.0
13 SEQ ID NO 18
14 LENGTH: 185
15
16 TYPE: PRT
17 ORGANISM: Artificial sequence
18 FEATURE:
19 NAME/KEY: synthetically generated
20 LOCATION: (1)...(185)
21 OTHER INFORMATION: human sequence predicted using an alignment algorithm which
22 OTHER INFORMATION: predicts presence of alternatively spliced exons for a prote
23 OTHER INFORMATION: interest in a stretch of genomic DNA
24 FEATURE:
25 NAME/KEY: VARIANT
26 LOCATION: (1)...(185)
27 OTHER INFORMATION: Xaa = Any Amino Acid
28 US-09-128-155-18

```

	Query Match	96.6%	Score 473.5;	DB 3;	Length 185;
	Best Local Similarity	41.8%;	Pred. NC .3;e-48;		
Matches	90;	Conservative	3;	Mismatches 4;	Indels 1; Gaps 1
OY	68 LASLSASAKSGSPILIGSKGFEFLDYDKRKGSHSLQTKKEKMLKLAAOKESARRP	127			
Dd	71 LSIQRSSAKSGPIPLGVSKGEFLLCDKRKGSHSRLQ-KETLMKLAAOKESARRP	129			
OY	128 FIFYPAGVGSNNMLESAAHPGWFICTSCMCNEPYVD	165			
Dd	130 FIFYPAGVGSNNMLESAAHPGMWFICTSCMCNEPVGLXN	167			

RESULT 9
 US-08-790-032-2
 ? Sequence 2, Application US/08790032
 ? Patent No.: 5863769
 ? GENERAL INFORMATION:
 ? APPLICANT: Young, Peter
 ? TITLE OF INVENTION: Interleukin-1 Receptor Antagonist
 ? TITLE OF INVENTION: Beta (IL-1RA_)
 ? NUMBER OF SEQUENCES: 2
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: SmithKline Beecham Corporation
 ? STREET: 709 Swedeland Road
 ? CITY: King of Prussia
 ? STATE: PA
 ? COUNTRY: USA
 ? ZIP: 19406-0939
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Diskette
 ? COMPUTER: IBM Compatible
 ? OPERATING SYSTEM: DOS
 ? SOFTWARE: FASTSEQ for Windows Version 2.0
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/790_032
 ? FILING DATE: 28-JAN-1997
 ? CLASSIFICATION: 536
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER:
 ? FILING DATE:
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Schreck, Patricia A
 ? REGISTRATION NUMBER: 33,777
 ? REFERENCE/DOCKET NUMBER: A7G50051


```
;; PRIOR FILING DATE: 1999-07-07
;; PRIOR APPLICATION NUMBER: PCT/US99/04291
;; PRIOR FILING DATE: 1999-04-05
;; PRIOR APPLICATION NUMBER: US 09/287,210
;; PRIOR FILING DATE: 1999-04-05
;; PRIOR APPLICATION NUMBER: US 09/251,370
;; PRIOR FILING DATE: 1999-02-17
;; PRIOR APPLICATION NUMBER: US 09/229,591
;; PRIOR FILING DATE: 1999-01-13
;; PRIOR APPLICATION NUMBER: US 09/127,698
;; PRIOR FILING DATE: 1998-07-31
;; PRIOR APPLICATION NUMBER: US 09/099,818
;; PRIOR FILING DATE: 1998-06-19
;; PRIOR APPLICATION NUMBER: US 09/082,364
;; PRIOR FILING DATE: 1998-05-20
;; PRIOR APPLICATION NUMBER: US 09/079,909
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: US 09/055,010
;; PRIOR FILING DATE: 1998-04-03
;; NUMBER OF SEQ ID NOS: 30
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 5
;; LENGTH: 155
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-417-455-5
```

```
Query Match          17.0%; Score 172.5; DB 4; Length 155;
Best Local Similarity 33.6%; Pred. No. 1.3e-12;
Matches 51; Conservative 17; Mismatches 47; Indels 37; Gaps 6;
```

```
QY 34 FSIHDDHRYLVLDGSLIAPDPKNYIRPEIFALASSLSASAERG----- 80
DB 9 FRKDSALAKVLYLHNQ-----LAGGLHAGKYIKGEISVYPRRWLDA 52
QY 81 --SPILLGVSKGEFCLYCDKDGQSHPSQLKKEKLMKL-AAOKESARRPFIYRAOYGS 137
DB 53 SLSPVILGVQGSQCLSC--GVGQ--EPTLTLEPVNIMELYLGAKE--KSFIFYRRDMGL 107
QY 138 WNMLESAAHPGWFICTSCNCPNEPVGTDKFEN 169
DB 108 TSFESAAYPGWFLCTVPEADQPVRLTQLPEN 139
```

```
RESULT 13
US-09-348-942-5
;; Sequence 5, Application US/09348942
;; Patent No. 6337072
;; GENERAL INFORMATION:
;; APPLICANT: John Ford
;; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
;; FILE REFERENCE: 28110/35801
;; CURRENT APPLICATION NUMBER: US/09/348,942
;; EARLIER FILING DATE: 1999-07-07
;; EARLIER APPLICATION NUMBER: PCT/US99/04291
;; EARLIER FILING DATE: 1999-04-05
;; EARLIER APPLICATION NUMBER: US 09/287,210
;; EARLIER FILING DATE: 1999-04-05
;; EARLIER APPLICATION NUMBER: US 09/251,370
;; EARLIER FILING DATE: 1999-02-17
;; EARLIER APPLICATION NUMBER: US 09/229,591
;; EARLIER FILING DATE: 1999-01-13
;; EARLIER APPLICATION NUMBER: US 09/127,698
;; EARLIER FILING DATE: 1998-07-31
;; EARLIER APPLICATION NUMBER: US 09/099,818
;; EARLIER FILING DATE: 1998-06-19
;; EARLIER APPLICATION NUMBER: US 09/082,364
;; EARLIER FILING DATE: 1998-05-20
;; EARLIER APPLICATION NUMBER: US 09/079,909
;; EARLIER FILING DATE: 1998-05-15
;; EARLIER APPLICATION NUMBER: US 09/055,010
;; EARLIER FILING DATE: 1998-04-03
;; NUMBER OF SEQ ID NOS: 30
```

```
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 5
;; LENGTH: 155
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-348-942-5
```

```
Query Match          17.0%; Score 172.5; DB 4; Length 155;
Best Local Similarity 33.6%; Pred. No. 1.3e-12;
Matches 51; Conservative 17; Mismatches 47; Indels 37; Gaps 6;
```

```
QY 34 FSIHDDHRYLVLDGSLIAPDPKNYIRPEIFALASSLSASAERG----- 80
DB 9 FRKDSALAKVLYLHNQ-----LAGGLHAGKYIKGEISVYPRRWLDA 52
QY 81 --SPILLGVSKGEFCLYCDKDGQSHPSQLKKEKLMKL-AAOKESARRPFIYRAOYGS 137
DB 53 SLSPVILGVQGSQCLSC--GVGQ--EPTLTLEPVNIMELYLGAKE--KSFIFYRRDMGL 107
QY 138 WNMLESAAHPGWFICTSCNCPNEPVGTDKFEN 169
DB 108 TSFESAAYPGWFLCTVPEADQPVRLTQLPEN 139
```

```
RESULT 14
US-09-316-081-5
;; Sequence 5, Application US/09316081
;; Patent No. 6339141
;; GENERAL INFORMATION:
;; APPLICANT: Ballinger, Dennis G.
;; APPLICANT: Pace, Ann M.
;; TITLE OF INVENTION: Interleukin-1 Hy2 Materials and Methods
;; FILE REFERENCE: 28110/35659
;; CURRENT APPLICATION NUMBER: US/09/316,081
;; EARLIER FILING DATE: 1999-05-20
;; NUMBER OF SEQ ID NOS: 11
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 5
;; LENGTH: 155
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-316-081-5
```

```
Query Match          17.0%; Score 172.5; DB 4; Length 155;
Best Local Similarity 33.6%; Pred. No. 1.3e-12;
Matches 51; Conservative 17; Mismatches 47; Indels 37; Gaps 6;
```

```
QY 34 FSIHDDHRYLVLDGSLIAPDPKNYIRPEIFALASSLSASAERG----- 80
DB 9 FRKDSALAKVLYLHNQ-----LAGGLHAGKYIKGEISVYPRRWLDA 52
QY 81 --SPILLGVSKGEFCLYCDKDGQSHPSQLKKEKLMKL-AAOKESARRPFIYRAOYGS 137
DB 53 SLSPVILGVQGSQCLSC--GVGQ--EPTLTLEPVNIMELYLGAKE--KSFIFYRRDMGL 107
QY 138 WNMLESAAHPGWFICTSCNCPNEPVGTDKFEN 169
DB 108 TSFESAAYPGWFLCTVPEADQPVRLTQLPEN 139
```

```
RESULT 15
US-09-578-458-5
;; Sequence 5, Application US/09578458
;; Patent No. 6365726
;; GENERAL INFORMATION:
;; APPLICANT: Ballinger, Dennis G.
;; APPLICANT: Ford, John
;; APPLICANT: Ho, Alice
;; APPLICANT: Lin, Hai Shan
;; APPLICANT: Pace, Ann M.
;; TITLE OF INVENTION: Interleukin-1 Hy2 Materials and Methods
;; FILE REFERENCE: 28110/36479
;; CURRENT APPLICATION NUMBER: US/09/578,458
```


OY	64	AGAGGTC	CCAAAGGTGAAGAACTTAAACCCGAAAGAAATTCAGATTCATATACCGAGATAC	12
Dd	199	ACAAGTCC	AAAGGTGAAGAACTTAAACCCGAAAGAAATTCAGATTCATATACCGAGATAC	25
OY	124	AAATACTG	TGCTCGGACCTCTGGAAATCTCATAGCACTTCAGATAAAAACTACATACGC	18
Dd	259	AAATACTG	TGCTCGGACCTCTGGAAATCTCATAGCACTTCAGATAAAAACTACATACGC	31
OY	184	CCGAGATCT	TTCTTTGCATATACCTTCATCTTGAGCTCAGCCTCTCGGGAGAAAGAAAGT	24
Dd	319	CCAGAGATCT	TTCTTTGCATATACCTTCATCTTGAGCTCAGCCTCTCGGGAGAAAGAAAGT	37
OY	244	CCGATTCCT	CTCGGGGGTCTCTAAAGGGAGTTTGTCTACTGTGACAAGATTAAGGA	30
Dd	379	CCGATTCCT	CTCGGGGGTCTCTAAAGGGAGTTTGTCTACTGTGACAAGATTAAGGA	43
OY	304	CAAAATCAT	CCATCCCTTAGCTGAGAAGAGGAAGAACTGATGAAGCTGGCTGCCAAAAG	36
Dd	439	CAAAATCAT	CCATCCCTTAGCTGAGAAGAGGAAGAACTGATGAAGCTGGCTGCCAAAAG	49
OY	364	GAATCAGAC	AGCCGGCCCTTCATCTTTTATAGGCTCAGGTGGGCTCTCGAAACTGCTG	42
Dd	499	GAATCAGAC	AGCCGGCCCTTCATCTTTTATAGGCTCAGGTGGGCTCTCGAAACTGCTG	55
OY	424	GAGTCGGC	GGCTCACCCCGGATAGTTCATCTGCACCTCTCGCAATTTGTAATGAGCCTGT	48
Dd	559	GAGTCGGC	GGCTCACCCCGGATAGTTCATCTGCACCTCTCGCAATTTGTAATGAGCCTGT	61

QY 484 GGGGTGACAGATAAATTTGAGACAGAAACATGATTTTCATTTCCAGCTTGC 543
DB 619 GGGGTGACAGATAAATTTGAGACAGAAACATGATTTTCATTTCCAGCTTGC 678
QY 544 AAAGCTGAATGAGCCCAAGTGAAGTCAAGCTTATG 579
DB 679 AAAGCTGAATGAGCCCAAGTGAAGTCAAGCTTATG 714

RESULT 2
US-09-128-155-1
Sequence 1, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:

APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 989
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (356)...(889)
US-09-128-155-1

Query Match
Best Local Similarity 98.0%; Score 395.2; DB 3; Length 989;
Matches 400; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 172 AACTACATAGCCCGAGAGATCTTTGATTAAGCTTCATCTGAGCTCAGCTCTGCG 231
DB 485 AATTTGTTACACAAAGATCTTTGATTAAGCTTCATCTGAGCTCAGCTCTGCG 544
QY 232 GAGAAAGAGTCCGATCTCTCGGGGCTCTAAAGGGAGTTTGTCTACTGTGAC 291
DB 545 GAGAAAGAGTCCGATCTCTCGGGGCTCTAAAGGGAGTTTGTCTACTGTGAC 604
QY 292 AAGGATTAAGGACAAAGTCAATCCCTTCAGCTGAAGAGGAGAACTGATGAAGCTG 351
DB 605 AAGGATTAAGGACAAAGTCAATCCCTTCAGCTGAAGAGGAGAACTGATGAAGCTG 664
QY 352 GCTGCCCAAAAGATGACAGCGCGGCTTCATCTTTTAAGGGCTCAGGTGGCTCC 411
DB 665 GCTGCCCAAAAGATGACAGCGCGGCTTCATCTTTTAAGGGCTCAGGTGGCTCC 724
QY 412 TGAACATGCTGAGTGGCGGCTCACCCGAGTGGTTCATCTGACCTCCGCAATGT 471
DB 725 TGAACATGCTGAGTGGCGGCTCACCCGAGTGGTTCATCTGACCTCCGCAATGT 784
QY 472 AATGAGCTGTTGGGCTGACAGATAATTTGAGACAGGAAACATTTGATTTT 531
DB 785 AATGAGCTGTTGGGCTGACAGATAATTTGAGACAGGAAACATTTGATTTT 844
QY 532 CAACCAATTTGCAAGTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 579
DB 845 CAACCAATTTGCAAGTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 892

RESULT 3
US-09-128-155-10
Sequence 10, Application US/09128155
Patent No. 6117654

GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 408
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(408)
US-09-128-155-10

Query Match
Best Local Similarity 98.0%; Score 392.2; DB 3; Length 408;
Matches 397; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 172 AACTACATAGCCCGAGAGATCTTTGATTAAGCTTCATCTGAGCTCAGCTCTGCG 231
DB 4 AATTTGTTACACAAAGATCTTTGATTAAGCTTCATCTGAGCTCAGCTCTGCG 63
QY 232 GAGAAAGAGTCCGATCTCTCGGGGCTCTAAAGGGAGTTTGTCTACTGTGAC 291
DB 64 GAGAAAGAGTCCGATCTCTCGGGGCTCTAAAGGGAGTTTGTCTACTGTGAC 123
QY 292 AAGGATTAAGGACAAAGTCAATCCCTTCAGCTGAAGAGGAGAACTGATGAAGCTG 351
DB 124 AAGGATTAAGGACAAAGTCAATCCCTTCAGCTGAAGAGGAGAACTGATGAAGCTG 183
QY 352 GCTGCCCAAAAGATGACAGCGCGGCTTCATCTTTTAAGGGCTCAGGTGGCTCC 411
DB 184 GCTGCCCAAAAGATGACAGCGCGGCTTCATCTTTTAAGGGCTCAGGTGGCTCC 243
QY 412 TGAACATGCTGAGTGGCGGCTCACCCGAGTGGTTCATCTGACCTCCGCAATGT 471
DB 244 TGAACATGCTGAGTGGCGGCTCACCCGAGTGGTTCATCTGACCTCCGCAATGT 303
QY 472 AATGAGCTGTTGGGCTGACAGATAATTTGAGACAGGAAACATTTGATTTT 531
DB 304 AATGAGCTGTTGGGCTGACAGATAATTTGAGACAGGAAACATTTGATTTT 363
QY 532 CAACCAATTTGCAAGTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 576
DB 364 CAACCAATTTGCAAGTGAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGT 408

RESULT 4
US-09-128-155-6
Sequence 6, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6

Db 159197 TCAGCGATTAG 159207

RESULT 7

US-08-790-032-1

; Sequence 1, Application US/08790032

; Patent No. 5863769

; GENERAL INFORMATION:

; APPLICANT: Young, Peter

; TITLE OF INVENTION: Interleukin-1 Receptor Antagonist

; TITLE OF INVENTION: Beta (IL-1RA_)

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation

; STREET: 709 Swedeland Road

; CITY: King of Prussia

; STATE: PA

; COUNTRY: USA

; ZIP: 19406-0939

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/790.032

; FILING DATE: 28-JAN-1997

; CLASSIFICATION: 536

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Schreck, Patricia A

; REGISTRATION NUMBER: 33,777

; REFERENCE/DOCKET NUMBER: ATG50051

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-270-5031

; TELEFAX: 610-270-5090

; TELEX:

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1183 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; US-08-790-032-1

Query Match 8.8%; Score 51.2; DB 2; Length 1183;

Best Local Similarity 48.9%; Pred. No. 4.1e-07;

Matches 227; Conservative 0; Mismatches 228; Indels 9; Gaps 3;

QY 88 AACCCGAGAAATTCAGATTCATGACGAGATCCAGCAAGATGAGTGGCTGAGCTGGG 147
DB 135 AAACCTATTACTGGAGCTTTATATGATTTGAATCAGCAAGTGTGACCTTCAGGGTCAG 194
QY 148 AATCTATAGCAGTTCCAGATTAATAAATACTACATACGCCAGAGATCTTTGCAATTAGCC 207
DB 195 AACCTTGTGGCAGTTCCAGCAAGATGAGTGTGACCCAG---TCAGTGTGCTGTATTC 251
QY 208 TCATCTTGTAGCTCAGCTCTGCGGAGAAAGAGATCCGATTCCTCTGGGGTCTCTAAA 267
DB 252 ACATGCAAGTATCCAGAGAGCTTTGAGCAAGGAGGAGATCCCATTTATTGGAATC 311
QY 268 GGGGAGTTTGTCTACTGTGACAGAGATAAGACAAATGATCCATCTCCCTTCAGCTG 327
DB 312 CAGAAATCCAGAAATGTGTTTGTATTGTAGAGAGGTTGGAGAACCCACATTCAGCTA 371
QY 328 AAGAAGAGAAATGATGAGTGGCTGCCCAAAAGAGAAATGAGACGCGCCCTTATC 387
DB 372 AAGAAGAGAAATGATGATCTGTATGTCCCAACCCGAGCCCTGTGAAA---CCCTTCCTT 428
QY 388 TTTTATAGGGCTCAGGTGGGCTCTGTGAACATGCTGAGTGGGCGGCTCACCCCGATGG 447

Db 429 TTCTACCGTGCAGAGACTGGTAGGACCTCCACCCCTTGAGTCTGTGGCTCCCGGACTGG 488

QY 448 TTCAATGACACCTCCTCGCATTTGTAATGAGCCTGTGGGTGACAGATAAATTTGAGAAC 507

Db 489 TTCAATG---CCTCCTCCAGAGAGACCGCATTCATCTGACTTCGACATTCGAGCTGGGAG 545

QY 508 AGGAACCATTTGATTTTCATTTCCAAACGATTGCAACCTGA 551

Db 546 TCATACACACTGCTTGAATTAATTAATGATGACTCA 589

RESULT 8

US-09-069-619-1

; Sequence 1, Application US/09069619

; Patent No. 6054559

; GENERAL INFORMATION:

; APPLICANT: Young, Peter and Lisa Marshall

; TITLE OF INVENTION: Interleukin-1 Receptor Antagonist

; TITLE OF INVENTION: Beta (IL-1RA_)

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation

; STREET: 709 Swedeland Road

; CITY: King of Prussia

; STATE: PA

; COUNTRY: USA

; ZIP: 19406-0939

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/069.619

; FILING DATE: Herewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/007,464; and 08/790,032

; FILING DATE: filed 14-JAN-1998; and 28-JAN-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Han, William, T.

; REGISTRATION NUMBER: 34,344

; REFERENCE/DOCKET NUMBER: ATG50051-2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-270-5219

; TELEFAX: 610-270-5090

; TELEX:

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1183 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; US-09-069-619-1

Query Match 8.8%; Score 51.2; DB 3; Length 1183;

Best Local Similarity 48.9%; Pred. No. 4.1e-07;

Matches 227; Conservative 0; Mismatches 228; Indels 9; Gaps 3;

QY 88 AACCCGAGAAATTCAGATTCATGACGAGATCCAGCAAGATGAGTGGCTGAGCTGGG 147
DB 135 AAACCTATTACTGGAGCTTTATATGATTTGAATCAGCAAGTGTGACCCCTTCAGGGTCAG 194
QY 148 AATCTATAGCAGTTCCAGATTAATAAATACTACATACGCCAGAGATCTTTGCAATTAGCC 207
DB 195 AACCTTGTGGCAGTTCCAGCAAGATGAGTGTGACCCAG---TCAGTGTGCTGTATTC 251
QY 208 TCATCTTGTAGCTCAGCTCTGCGGAGAAAGAGATCCGATTCCTCTGGGGTCTCTAAA 267
DB 252 ACATGCAAGTATCCAGAGAGCTTTGAGCAAGGAGGAGATCCCATTTATTGGAATC 311

[illegible]

RESULT 11
 US-09-000-630C-25
 Sequence 25 Application US/09000630C
 Patent No. 6018029
 GENERAL INFORMATION:
 APPLICANT: Fuller, Gerald M
 APPLICANT: Fuentes, Nelson L.
 TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor
 TITLE OF INVENTION: Antagonist
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Douglas C Murodock/ Bradley, Arant, Rose & White
 STREET: 2001 Park Place, Suite 1400
 CITY: Birmingham
 STATE: Alabama
 COUNTRY: USA
 ZIP: 35203-2736
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 Inch,
 COMPUTER: IBM compatible
 OPERATING SYSTEM: Microsoft Windows
 SOFTWARE: Wordperfect 6.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/000.630C
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/862,730
 FILING DATE:
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 537 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: mouse IL-1ra DNA sequence
 US-09-000-630C-25

Query Match	6.3%	Score 36.6	DB 3	Length 537
Best Local Similarity	53.1%	Pred. No. 0.019	Mismatches 69	Indels 0
Matches 78	Conservative	0	Gaps	0
QY 357	CCAAAGGATTCAGCAGCGCGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCTTGGA	416		
Db 345	CAGAACAAAGAAAGAGACAGCGCTTACCTTACCTCCGCTGTAGAAAGGCCACACAC	404		
QY 417	CATGCTGGAGTGGGGGCTCACCCGAGTGTTCATCTGCACCTCCGCAATGTGTATYGA	476		
Db 405	CAGCTTGTGATCAGCTGCTGTCCAGGATGGTTCTCTGTACACACTAGAGGCTGACG	464		
QY 477	GCCGTTGGGGTGACAGATAATTGGA	503		
Db 465	TCTGTGTAGCTTACCACACACCGGA	491		

RESULT 12
 US-08-862-730C-25
 Sequence 25. Application US/08662730C
 Patent No. 6063600
 GENERAL INFORMATION:
 APPLICANT: Fuller, Gerald M
 APPLICANT: Fuentes, Nelson L.
 TITLE OF INVENTION: DNA Encoding Canine Interleukin-1 Receptor
 TITLE OF INVENTION: Antagonist
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Douglas C Murdock/Bradley, Arant, Rose & White
 STREET: 2001 Park Place, Suite 1400
 CITY: Birmingham
 STATE: Alabama
 COUNTRY: USA
 ZIP: 35203-2736
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch,
 COMPUTER: IBM compatible
 OPERATING SYSTEM: Microsoft Windows
 SOFTWARE: Wordperfect 6.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/862,730C
 FILING DATE: 5/23/97
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 537 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: mouse IL-1ra DNA sequence
 US-08-862-730C-25

Query Match	6.3%	Score 36.6	DB 3	Length 537
Best Local Similarity	53.1%	Pred. No. 0.019	Mismatches 69	Indels 0
Matches 78	Conservative	0	Gaps 0	
QY 357	CCAAAGGATCGACGCGGCCCTTCATCTTTATGAGGGCTCAGGTGGCTCTGGAA	416		
Db 345	CAGAAGCAAGAGAGACAGAGGGCTTACCTTCATCCGCTCTGAGAAAGGCCACAC	404		
QY 417	CATGCTGAGTGGGGGCTCACCCGGATGTTATCTTCGACCTTCGCAATTGTATGA	476		
Db 405	CAGCTTGAATCGACGCTGCTTCACAGATGGTTCCTCTGCACAACTAGAGGCTGACC	464		
QY 477	GCCGTGGGGTGACAGATAATTGA	503		
Db 465	TCTGTGAGCTTCCACACACCGGA	491		

RESULT 13
 US-09-647-826-1
 Sequence 1, Application US/09647826
 Patent No. 6437216
 GENERAL INFORMATION:
 APPLICANT: Duff, Gordon W.
 APPLICANT: Nicklin, Martin
 APPLICANT: Interleukin Genetics, Inc.
 TITLE OF INVENTION: TRANSGENIC MODELS OF INFLAMMATORY DISEASE
 FILE REFERENCE: MSA-003.01
 CURRENT APPLICATION NUMBER: US/09/647,826
 CURRENT FILING DATE: 2001-03-12
 PRIOR APPLICATION NUMBER: GB 9723835.6
 PRIOR FILING DATE: 1997-11-13
 NUMBER OF SEQ ID NOS: 2
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 1
 LENGTH: 6350
 TYPE: DNA
 ORGANISM: mouse
 US-09-647-826-1

Query Match	6.3%	Score 36.6	DB 4	Length 6350
Best Local Similarity	53.1%	Pred. No. 0.076	Mismatches 69	Indels 0
Matches 78	Conservative 0	Mismatches 69	Indels 0	Gaps 0
OY	357	CCAAAAGGAATCAGCAGCGCGGCCCTTCATCTTTTATAGGGCTCAGTGGGCTCTTGAA	416	
Db	4358	CAGAACAAGAAGAAGAACAGCGCTTACCTTCATCCGCTTGAGAAAGGCCCAACC	4417	
OY	417	CATGCTGAGTGTGGGGGCTCACCCGGATGTTCACTTGCACCTCTGCAATTGTAAATGA	476	
Db	4418	CAGCTTTAGTCAGTCGCTGCTTCACGAGATGGTTCCTGCAACAACATAGAGGCTGACGG	4477	
OY	477	GCCTTTGGGGTGACAGATAAATTGA	503	
Db	4478	TCTCTTGAGCCTCACCAACACACCGGA	4504	

```

RESULT 14
US-09-058-489-86
; Sequence 86, Application US/09058489
; Patent No. 6103886
; GENERAL INFORMATION:
; APPLICANT: Whitehead Institute for Biomedical Research
; APPLICANT: Lahn, Bruce
; APPLICANT: Page, David
; TITLE OF INVENTION: Genes in the No. 6103886-Recombining Region of
; TITLE OF INVENTION: the Y Chromosome
; FILE REFERENCE: WH197-08PA
; CURRENT APPLICATION NUMBER: US/09/058,489
; CURRENT FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/041,877
; EARLIER FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 2983
; TYPE: DNA
; ORGANISM: Human
US-09-058-489-86

```

	Query Match	6.1%;	Score 35.6;	DB 3;	Length 2983;
	Best Local Similarity	45.8%;	Pred. No. 0.11;	Mismatches 140;	Indels 0; Gaps 0;
	Matches 119;	Conservative 1;			
QY	2	TGTCAGGCTGTGATBAGGAGGGAACAGAACCAAAAGAAAGACAGCTTTAAGAAGCGCT	61		
Db	1156	TGACAGCCGGGAAAAAATAATTATTGACGACAGMAAGAACCAACTTTTGACAAGCGGT	1215		
QY	62	TAAAGAGTCCAAAGGTGAAGAACTTAACCCGAACTTAATTCAGATTCATGACCAAGATC	121		
Db	1216	TGGGTTTCAGTGTGAGAGGCACAGAGATGGCTCACAGTACAGAGATATTGTGTCAGGA	1275		
QY	122	ACCAAATGACTGGTCCCTGGGACTCTGGGAATCTCATBAGCAGTTCCAGATAAAACCTACATAC	181		
Db	1276	AGCAAAATGGCTTCACCCCACATCTTTATTCACAAAATCTCTCAGAAATAATCTCACTAA	1335		
QY	182	GCCCCAGAGATCTTCTTTGATTAAGCCTATCCTTTGAGTCCAGCCTCTGCCGAGAAAGAA	241		
Db	1336	ACCCAGAGGTGATGAAGAAGTRCAGAGAGCGCCTGAGACACAGCTGCAGCCGACAGACAGCA	1395		
QY	242	GTCGGATTCTCCTGGGGGCTC	261		
Db	1396	AGCTGGTTCTGCTCAGCGCC	1415		

RESULT 15
US-09-578-458-16
Sequence 16, Application US/09578458
Patent No. 6365756
GENERAL INFORMATION:
APPLICANT: Ballinger, Dennis G.
APPLICANT: Ford, John
APPLICANT: Ho, Alice

```

? APPLICANT: Lin, Hai Shan
? APPLICANT: Pace, Ann M.
? TITLE OF INVENTION: Interleukin-1 Hy2 Materials and Methods
? FILE REFERENCE: 28110/36479
? CURRENT APPLICATION NUMBER: US/09/578,458
? CURRENT FILING DATE: 2000-05-22
? PRIOR APPLICATION NUMBER: US 09/522,964
? PRIOR FILING DATE: 2000-03-10
? PRIOR APPLICATION NUMBER: US 09/316,086
? PRIOR FILING DATE: 1999-03-20
? NUMBER OF SEQ ID NOS: 20
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 16
? LENGTH: 4388
? TYPE: DNA
? ORGANISM: Mouse
? US-09-578-458-16

```

Query Match	6.1%	Score 35.6	DB 4	Length 4388
Best Local Similarity	50.0%	Pred. No. 0.13		
Matches	89	Conservative	0	Mismatches 89
				Indels 0
				Gaps 0
QY	382	TTCACTCTTTATATAGGGCTCAGGTGGGCTCTCGAACAATGCTGAGTGGCGGCTCACCCC	441	
Db	3775	TTACACCTTTTTCACAGAAAGCTTGGGAACTCGCTTCAAGGCTTGAGGCGTGTGCTCGCCT	3834	
QY	442	GGATGTTTCACTGCACCTCTCGCAATTGTATATAGGCGCTGTGGGTTGACAGATTAATTT	501	
Db	3835	GGCTGGTTCCTCTGTCGGCCAGCTAGCCACAGCGCCAGCTGAGCTCACCAAGAGAGT	3894	
QY	502	GAGAACGGAAACATCTGAATTTTCATTTCATTCACACAGATTTGCCAAAGCTGAATAAGACC	559	
Db	3895	GAACTTCACACCATCTGAATTTTACTTTGATGATGATGCTGTTAAGACAGCATTAAGGC	3952	

Search completed: May 3, 2003, 06:31:32Z
Job time : 203 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 3, 2003, 04:04:12 ; Search time 1797 Seconds

(without alignments)
9377.031 Million cell updates/sec

Title: US-09-876-790-1

Perfect score: 579

Sequence: 1 atgcagctgtatagagag.....ccagtgcagctagtag 579

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: gb.ba:*
2: gb.htg:*
3: gb.in:*
4: gb.om:*
5: gb.ov:*
6: gb.pat:*
7: gb.ph:*
8: gb.pl:*
9: gb.pr:*
10: gb.ro:*
11: gb.sts:*
12: gb.sy:*
13: gb.un:*
14: gb.vi:*
15: em.ba:*
16: em.fun:*
17: em.hum:*
18: em.in:*
19: em.mu:*
20: em.om:*
21: em.or:*
22: em.ov:*
23: em.pat:*
24: em.ph:*
25: em.pl:*
26: em.ro:*
27: em.sts:*
28: em.un:*
29: em.vi:*
30: em.htg.hum:*
31: em.htg.in:*
32: em.htg.other:*
33: em.htg.mus:*
34: em.htg.pla:*
35: em.htg.rtd:*
36: em.htg.mam:*
37: em.htg.vrt:*
38: em.sv:*
39: em.htgo.hum:*
40: em.htgo.mus:*
41: em.htgo.other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	579	100.0	579	9	AF201832	AF201832 Homo sapi
2	517.8	89.4	594	9	AY071840	AY071840 Homo sapi
3	512.8	88.6	657	9	AF251119	AF251119 Homo sapi
4	512.8	88.6	760	9	BC020637	BC020637 Homo sapi
5	512.8	88.6	787	9	AF167368	AF167368 Homo sapi
6	512.8	88.6	793	9	AF200496	AF200496 Homo sapi
7	512.8	88.6	802	6	AR183757	AR183757 Homo sapi
8	512.8	88.6	817	9	AF251118	AF251118 Homo sapi
9	512.8	88.6	847	6	AX133934	AX133934 Sequence
10	512.8	88.6	855	6	AX133936	AX133936 Sequence
11	509.6	88.0	630	6	AX048211	AX048211 Sequence
12	504	87.0	754	6	AX092410	AX092410 Sequence
13	396.6	68.5	537	9	AF251120	AF251120 Homo sapi
14	394	68.0	474	9	AY071841	AY071841 Homo sapi
15	310.8	53.7	575	6	AX133932	AX133932 Sequence
16	251	43.4	154214	9	AC079753	AC079753 Homo sapi
17	178	30.7	248	6	AX133933	AX133933 Sequence
18	113.2	19.6	118	6	AX133931	AX133931 Sequence
19	68.8	11.9	187395	2	AC096974	AC096974 Rattus no
20	57.6	9.9	187395	2	AC096974	AC096974 Rattus no
21	51.2	8.8	648	10	AY071842	AY071842 Mus muscu
22	51.2	8.8	1073	6	AX207820	AX207820 Sequence
23	51.2	8.8	1177	9	AF206696	AF206696 Homo sapi
24	51.2	8.8	1183	6	AR212173	AR212173 Sequence
25	51.2	8.8	1183	6	E54910	E54910 Interleukin
26	51.2	8.8	1183	6	AF200492	AF200492 Homo sapi
27	48.6	8.4	520	6	AX193587	AX193587 Sequence
28	48.6	8.4	585	6	AX052581	AX052581 Sequence
29	48.6	8.4	585	6	AF201833	AF201833 Homo sapi
30	48.6	8.4	1244	6	AX167128	AX167128 Sequence
31	47.6	8.2	329	6	AX193643	AX193643 Sequence
32	47.6	8.2	477	9	AF201831	AF201831 Homo sapi
33	43.8	7.6	1321	6	AX454724	AX454724 Sequence
34	43.8	7.6	1321	6	AX491202	AX491202 Sequence
35	41.4	7.2	27236	3	CEY32P6A	AI021474 Caenorhab
36	41.4	7.2	36879	2	CEK07H11	Z81566 Caenorhabdi
37	40.6	7.0	465	6	AX080399	AX080399 Sequence
38	40.6	7.0	468	6	AX069335	AX069335 Sequence
39	40.6	7.0	471	10	AF230378	AF230378 Mus muscu
40	40.6	7.0	1283	6	AF200495	AF200495 Mus muscu
41	40.6	7.0	1284	6	AX080392	AX080392 Sequence
42	40.6	7.0	1284	10	MMU250429	AI250429 Mus muscu
43	40.6	7.0	8032	6	AX069334	AX069334 Sequence
44	40.6	7.0	201610	10	AL732430	AL732430 Mouse DNA
45	39.8	6.9	182845	2	AC110438	AC110438 Rattus no

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE
AF201832	AF201832	Homo sapiens FIIL zeta mRNA, complete cds.	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.
AF201832	AF201832	579 bp mRNA linear PRI 16-JAN-2000	AF201832	AF201832.1	GI:6694391	Homo sapiens.	Homo sapiens.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	1 (bases 1 to 579)	Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garaka,K.E. and Sims,J.E.

Db	Accession	Source	Organism	Reference	Journal	Remark
Db	322	CCGATTCCTCCGAGGGGGGTCTCTAAAGGGGAGTTTGTCTCTACTGTGACAAAGATAAAGGA	381			
QY	304	CAAAAGTCATCCATCCCTTCCTTACGCTGAAGAGAGAGAAACTGATGAAGCTGGCTGCCAAAG	363			
Db	382	CAAAAGTCATCCATCCCTTCCTTACGCTGAAGAGAGAAACTGATGAAGCTGGCTGCCAAAG	441			
QY	364	GAATCAGACAGCCCGGCCCTTCATCTTTATATAGGGCTCAGGTGGGCTCCTGGAAATGCTG	423			
Db	442	GAATCAGACAGCCCGGCCCTTCATCTTTATATAGGGCTCAGGTGGGCTCCTGGAAATGCTG	501			
QY	424	GAGTCGGGCGGCTCAACCCCGATGTTTCATCTGCAACCTTCCTGCAATTGTAATGAGCTGT	483			
Db	502	GAGTCGGGCGGCTCAACCCCGATGTTTCATCTGCAACCTTCCTGCAATTGTAATGAGCTGT	561			
QY	484	GGGCTGACAGTAATTTTGAGAAACAGGAAACATTTGATTTCAATTCACCAAGTTTGC	543			
Db	562	GGGCTGACAGTAATTTTGAGAAACAGGAAACATTTGATTTCAATTCACCAAGTTTGC	621			
QY	544	AAAGCTGAATGAGACCCCGATGAGTGCAGCTGATG	579			
Db	622	AAAGCTGAATGAGACCCCGATGAGTGCAGCTGATG	657			
RESULT 4						
LOCUS	BC020637	760 bp	mRNA	linear	PRI 08-JAN-2002	
DEFINITION	Homo sapiens, clone MGC:22276 IMAGE:4731213, mRNA, complete cds.					
ACCESSION	BC020637					
VERSION	BC020637.1	GI:18088327				
KEYWORDS	MGC.					
SOURCE	Homo sapiens.					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
REFERENCE	1 (bases 1 to 760)					
AUTHORS	Strausberg, R.					
TITLE	Direct Submission					
JOURNAL	Submitted (03-JAN-2002) National Institutes of Health, Mammalian					
	Gene Collection (MGC), Cancer Genomics Office, National Cancer					
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,					
	USA					
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov					
COMMENT	Contact: MGC help desk					
	Email: cgapds-remail.nih.gov					
	Tissue Procurement: CLONTECH					
	cDNA Library Preparation: CLONTECH Laboratories, Inc.					
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)					
	DNA Sequencing by: Sequencing Group at the Stanford Human Genome					
	Center, Stanford University School of Medicine, Stanford, CA 94305					
	Web Site: http://www.shgc.stanford.edu					
	Contact: (Dickson, Mark) mcdepaxil.stanford.edu					
	Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,					
	R. M.					
	Clone distribution: MGC clone distribution information can be found					
	through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov					
	Series: IRAL Plate: 37 Row: h Column: 22.					
	Location/Qualifiers					
	1. 760					
FEATURES						
source						
	/organism="Homo sapiens"					
	/db_xref="taxon:9606"					
	/clone="MGC:22276 IMAGE:4731213"					
	/tissue_type="Placenta"					
	/clone_lib="NIH-MGC_79"					
	/lab_host="DH10B"					
	/note="Vector: pDNR-LIB"					
	4. 660					
	/codon_start=1					
	/product="unknown (protein for MGC:22276)"					
	/protein_id="AAH20637.1"					
	/db_xref="GI:18088328"					
	/translation="MSFVGGSEGVKMGSEDEKDEPOCCLEDAVSPLEPEGPSIPAMN					
	FVHSIPVYKNIINPKKFSIHDDHVLVLDSGNLIIVDPKNIIRFELFALASLSAS					

BASE COUNT 240 a 178 c 175 g 167 t
 ORIGIN
 AERGSFILLGVSKGFECLYCDKDGSHPSLOLKEKIMLAOKESARPFIFYRAO
 VGSWMNLESAHPGWFICTSCNENPEVGTDFENRKHIEFSFQPVCAKEMSPSEVSD

Query Match 88.6%; Score 512.8; DB 9; Length 760;
 Best Local Similarity 99.6%; Pred. No. 4e-148;
 Matches 514; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 AGAGGTCCAAAGGTGAAGAACTTAACCCGGAAGAAATTTGAGCTTTATACCAAGATCAC 123
 DB 145 ACAAGTCCAAAGGTGAAGAACTTAACCCGGAAGAAATTTGAGCTTTATACCAAGATCAC 204
 QY 124 AAAGTACTGCTCTGAGACTCTGGGAATCTCATAGAGTCCAGATPAAAACTACATACGC 183
 DB 205 AAAGTACTGCTCTGAGACTCTGGGAATCTCATAGAGTCCAGATPAAAACTACATACGC 264
 QY 184 CCAGAGATCTCTTTGCAATTAAGCTTATCCTTGAGCTCAGCCTTGCGGAGAAAGAGT 243
 DB 265 CCAGAGATCTCTTTGCAATTAAGCTTATCCTTGAGCTCAGCCTTGCGGAGAAAGAGT 324
 QY 244 CCAGATCTCTGAGGCTCTCTAAGGGAGTTTGTCTACTGACAGATATAAGGA 303
 DB 325 CCAGATCTCTGAGGCTCTCTAAGGGAGTTTGTCTACTGACAGATATAAGGA 384
 QY 304 CAAAGTCAATCCATCCCTTACAGCTGAAGAGAGAAATGATAGCTGCTGCCAAAG 363
 DB 385 CAAAGTCAATCCATCCCTTACAGCTGAAGAGAGAAATGATAGCTGCTGCCAAAG 444
 QY 364 GAATCAGACGCGCGGCTCTCATCTTTATAGGCTCAGTGGGCTCCTGGAACATGCTG 423
 DB 445 GAATCAGACGCGCGGCTCTCATCTTTATAGGCTCAGTGGGCTCCTGGAACATGCTG 504
 QY 424 GAGTCGGCGGCTCACCCCGGATGTTTCATCTGACCTCTGCAATTTGATAGCTGTT 483
 DB 505 GAGTCGGCGGCTCACCCCGGATGTTTCATCTGACCTCTGCAATTTGATAGCTGTT 564
 QY 484 GGGGTGACAGATTAATTTGAGAACAGAGAAACATTTGATTTCAATTTCAACCATTTGC 543
 DB 565 GGGGTGACAGATTAATTTGAGAACAGAGAAACATTTGATTTCAATTTCAACCATTTGC 624
 QY 544 AAAGCTGAATGAGCCCGAGTGAAGTCAAGCATTAG 579
 DB 625 AAAGCTGAATGAGCCCGAGTGAAGTCAAGCATTAG 660

RESULT 5
 AF167368 787 bp mRNA Linear PRI 03-NOV-2000
 LOCUS AF167368
 DEFINITION Homo sapiens IL-1X protein mRNA, complete cds.
 ACCESSION AF167368
 VERSION AF167368.1 GI:11093527
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 787)
 AUTHORS Manoj, P.P., Mantovani, A. and Muzio, M.
 TITLE Direct Submission
 JOURNAL Submitted (09-JUL-1999) Immunology, IRMMN Mario Negri, Via-Eritrea:
 62, Milano 20157, Italy
 FEATURES
 Location/Qualifiers
 1..787
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /feature_type="cds" col="1" from="1" to="787" type="cds"/>

CDS

/note="similar to IL-1"
 /codon_start=1
 /product="IL-1X protein"
 /protein_id="AAG29344.1"

/db_xref="GI:11093528"
 /translation="MSFVGENSGYKMGSEDEKDEPOCCLEDPAGSPLEPGSLPTMN
 FVHTSPKVNINPKFESIHDDHRYVLVDGSLNLAAPDKNYIRPEIFFALASSLSAS
 AERGSFILLGVSKGFECLYCDKDGSHPSLOLKEKIMLAOKESARPFIFYRAO
 VGSWMNLESAHPGWFICTSCNENPEVGTDFENRKHIEFSFQPVCAKEMSPSEVSD

BASE COUNT 239 a 187 c 179 g 182 t
 ORIGIN

Query Match 88.6%; Score 512.8; DB 9; Length 787;
 Best Local Similarity 99.6%; Pred. No. 4e-148;
 Matches 514; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 AGAGTCCAAAGGTGAAGAACTTAACCCGGAAGAAATTTGAGCTTTATACCAAGATCAC 123
 DB 184 ACAAGTCCAAAGGTGAAGAACTTAACCCGGAAGAAATTTGAGCTTTATACCAAGATCAC 243
 QY 124 AAAGTACTGCTCTGAGACTCTGGGAATCTCATAGAGTCCAGATPAAAACTACATACGC 183
 DB 244 AAAGTACTGCTCTGAGACTCTGGGAATCTCATAGAGTCCAGATPAAAACTACATACGC 303
 QY 184 CCAGAGATCTCTTTGCAATTAAGCTTATCCTTGAGCTCAGCCTTGCGGAGAAAGAGT 243
 DB 304 CCAGAGATCTCTTTGCAATTAAGCTTATCCTTGAGCTCAGCCTTGCGGAGAAAGAGT 363
 QY 244 CCAGATCTCTGAGGCTCTCTAAGGGAGTTTGTCTACTGACAGATATAAGGA 303
 DB 364 CCAGATCTCTGAGGCTCTCTAAGGGAGTTTGTCTACTGACAGATATAAGGA 423
 QY 304 CAAAGTCAATCCATCCCTTACAGCTGAAGAGAGAAATGATAGCTGCTGCCAAAG 363
 DB 424 CAAAGTCAATCCATCCCTTACAGCTGAAGAGAGAAATGATAGCTGCTGCCAAAG 483
 QY 364 GAATCAGACGCGCGGCTCTCATCTTTATAGGCTCAGTGGGCTCCTGGAACATGCTG 423
 DB 484 GAATCAGACGCGCGGCTCTCATCTTTATAGGCTCAGTGGGCTCCTGGAACATGCTG 543
 QY 424 GAGTCGGCGGCTCACCCCGGATGTTTCATCTGACCTCTGCAATTTGATAGCTGTT 483
 DB 544 GAGTCGGCGGCTCACCCCGGATGTTTCATCTGACCTCTGCAATTTGATAGCTGTT 603
 QY 484 GGGGTGACAGATTAATTTGAGAACAGAGAAACATTTGATTTCAATTTCAACCATTTGC 543
 DB 604 GGGGTGACAGATTAATTTGAGAACAGAGAAACATTTGATTTCAATTTCAACCATTTGC 663
 QY 544 AAAGCTGAATGAGCCCGAGTGAAGTCAAGCATTAG 579
 DB 664 AAAGCTGAATGAGCCCGAGTGAAGTCAAGCATTAG 699

RESULT 6
 AF200496 793 bp mRNA Linear PRI 11-MAY-2000
 LOCUS AF200496
 DEFINITION Homo sapiens Interleukin-1 homolog 4 mRNA, complete cds.
 ACCESSION AF200496
 VERSION AF200496.1 GI:7769119
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 793)
 AUTHORS Kumar, S., McDonnell, P.C., Lehr, R., Tierney, L., Tzimas, M.N.,
 Griswold, D.E., Capper, E.A., Tal-Singer, R., Wells, G.I., Doyle, M.L.
 and Young, P.R.
 TITLE Identification and initial characterization of four novel members
 of the Interleukin-1 family
 JOURNAL J. Biol. Chem. 275 (14), 10308-10314 (2000)
 MEDLINE 20209405
 PUBMED 10744718
 REFERENCE 2 (bases 1 to 793)
 AUTHORS Kumar, S., McDonnell, P.C. and Young, P.R.
 TITLE Direct Submission

JOURNAL Submitted (01-NOV-1999) Bone and Cartilage Biology, UW 2109,
SmithKline Beecham Pharmaceuticals, 709 Swedeland Rd., King of
Prussia, PA 19406, USA

FEATURES
source Location/Qualifiers

1..793
/organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="mixed fetal lung, testes, B cells and colon"
49..705
/note="cytokine: hIL-1H4"

CDS
/codon_start=1
/product="Interleukin-1 homolog 4"
/protein_id="AAF69252.1"
/db_xref="GI:7769120"

/translation="MSFVGENGVKMGSEDEKDEPOCCLEDPAGSPLEPPSPLEPTN
FVHSKKNLNPKEFSIHDDHKLVLDSGLVLPKNTIREFIFALSSLSAS
AEKSPILLGVSGEFCYCDKDGKSHSLQLEKEMKLAAQESARPFIEYRAQ
VGSMMLESAAHPGWFICTSCNNEPVITDKFENRKHIEFSFQVCKAEMSPSEVSD
"

misc_feature 109..110

BASE COUNT 241 a 188 c 182 g 182 t
ORIGIN

Query Match 88.6%; Score 512.8; DB 9; Length 793;

Best Local Similarity 99.6%; Pred. No. 4e-148;
Matches 514; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 AGAGTCCAAAGGTGAAGAACTTAAACCCGAGAAATTCAGCATTCATGACGAGATCAC 123
DB 190 ACAAGTCCAAAGGTGAAGAACTTAAACCCGAGAAATTCAGCATTCATGACGAGATCAC 249
QY 124 AAGTACTGCTCTGGACCTGGGATCTCATGAGCTTCAGATTAAGAACTAATACATACGC 183
DB 250 AAGTACTGCTCTGGACCTGGGATCTCATGAGCTTCAGATTAAGAACTAATACATACGC 309
QY 184 CCAGAGATCTCTTTCATTAAGCTCATCTTTCAGCTCAGCTCCTCGGAGAAAGAGAT 243
DB 310 CCAGAGATCTCTTTCATTAAGCTCATCTTTCAGCTCAGCTCCTCGGAGAAAGAGAT 369
QY 244 CCATCTCTCTGGGGCTCTTAAAGGGAGTTTGTCTCTACTGTACAAAGATTAAGGA 303
DB 370 CCATCTCTCTGGGGCTCTTAAAGGGAGTTTGTCTCTACTGTACAAAGATTAAGGA 429
QY 304 CAAAGTCATCCATCCCTTCAGCTGAAGAGAGAACTGATGAGCTGGGCTGCCCAAAAG 363
DB 430 CAAAGTCATCCATCCCTTCAGCTGAAGAGAGAACTGATGAGCTGGGCTGCCCAAAAG 489
QY 364 GAATCAGACAGCGCGGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCTGGAACATGCTG 423
DB 490 GAATCAGACAGCGCGGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCTGGAACATGCTG 549
QY 424 GAGTGGCGGCTCAGCCCGGATGTTTCATCTGACCTCTGCAATTTGATGAGCTGTT 483
DB 550 GAGTGGCGGCTCAGCCCGGATGTTTCATCTGACCTCTGCAATTTGATGAGCTGTT 609
QY 484 GGGGTGACAGATTAATTTGAGAACAGAAACACATTTGATTTTCAACAGATTGGC 543
DB 610 GGGGTGACAGATTAATTTGAGAACAGAAACACATTTGATTTTCAACAGATTGGC 669
QY 544 AAGCTGAATGAGCCCGCAGTGAAGTTCAGGATTAG 579
DB 670 AAGCTGAATGAGCCCGCAGTGAAGTTCAGGATTAG 705

RESULT 7
LOCUS AR183757 802 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 1 from patent US 6342371.
ACCESSION AR183757
VERSION AR183757.1 GI:20227726
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 802)

AUTHORS McDonnell, P.C. and Young, P.R.

TITLE Interleukin-1 homologue, IL-1H4

JOURNAL Patent: US 6342371-A 1 29-JAN-2002;

FEATURES Location/Qualifiers

source 1..802
/organism="unknown"

BASE COUNT 243 a 190 c 185 g 184 t
ORIGIN

Query Match 88.6%; Score 512.8; DB 6; Length 802;

Best Local Similarity 99.6%; Pred. No. 4e-148;
Matches 514; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 AGAGTCCAAAGGTGAAGAACTTAAACCCGAGAAATTCAGCATTCATGACGAGATCAC 123
DB 190 ACAAGTCCAAAGGTGAAGAACTTAAACCCGAGAAATTCAGCATTCATGACGAGATCAC 258
QY 124 AAGTACTGCTCTGGACCTGGGATCTCATGAGCTTCAGATTAAGAACTAATACATACGC 183
DB 250 AAGTACTGCTCTGGACCTGGGATCTCATGAGCTTCAGATTAAGAACTAATACATACGC 318
QY 184 CCAGAGATCTCTTTCATTAAGCTCATCTTTCAGCTCAGCTCCTCGGAGAAAGAGAT 243
DB 319 CCAGAGATCTCTTTCATTAAGCTCATCTTTCAGCTCAGCTCCTCGGAGAAAGAGAT 378
QY 244 CCATCTCTCTGGGGCTCTTAAAGGGAGTTTGTCTCTACTGTGACAGAGATTAAGGA 303
DB 379 CCATCTCTCTGGGGCTCTTAAAGGGAGTTTGTCTCTACTGTGACAGAGATTAAGGA 438
QY 304 CAAAGTCATCCATCCCTTCAGCTGAAGAGAGAACTGATGAGCTGGGCTGCCCAAAAG 363
DB 439 CAAAGTCATCCATCCCTTCAGCTGAAGAGAGAACTGATGAGCTGGGCTGCCCAAAAG 498
QY 364 GAATCAGACAGCGCGGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCTGGAACATGCTG 423
DB 499 GAATCAGACAGCGCGGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCTGGAACATGCTG 558
QY 424 GAGTGGCGGCTCAGCCCGGATGTTTCATCTGACCTCTGCAATTTGATGAGCTGTT 483
DB 559 GAGTGGCGGCTCAGCCCGGATGTTTCATCTGACCTCTGCAATTTGATGAGCTGTT 618
QY 484 GGGGTGACAGATTAATTTGAGAACAGAAACACATTTGATTTTCAACAGATTGGC 543
DB 619 GGGGTGACAGATTAATTTGAGAACAGAAACACATTTGATTTTCAACAGATTGGC 678
QY 544 AAGCTGAATGAGCCCGCAGTGAAGTTCAGGATTAG 579
DB 679 AAGCTGAATGAGCCCGCAGTGAAGTTCAGGATTAG 714

RESULT 8
LOCUS AF251118 817 bp mRNA linear PRI 03-MAY-2001
DEFINITION Homo sapiens interleukin-1-related protein long isoform a mRNA,
complete cds; alternatively spliced.
ACCESSION AF251118
VERSION AF251118.1 GI:10185735
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 817)
AUTHORS Pan, G., Rissler, P., Mao, W., Baldwin, D.T., Zhong, A.W., Filvaroff, E.,
Yanamura, D., Lewis, L., Eigenbrodt, C., Henzel, W.J. and Vanden, R.
TITLE IL-1H, an interleukin 1-related protein that binds IL-18
receptor/IL-1Rrp
JOURNAL Cytokine 13 (1), 1-7 (2001)
MEDLINE 2106552
PUBMED 11145836

REFERENCE 2 (bases 1 to 817)
AUTHORS Pan, G., Baldwin, D. T., and Zhong, A. W.
TITLE Direct Submission
JOURNAL Submitted (03-APR-2000) Endocrinology, Genentech, Inc., 1 DNA Way,
South San Francisco, CA 94080, USA

FEATURES
source
1. 817
/organism="Homo sapiens"
/db_xref="taxon:9606"
73..729
/note="IL-1H; IL-1 family member; binds IL-18
receptor/IL-1Rcp; putative involvement in inflammation and
immune responses"
/product="interleukin-1-related protein long isoform a"
/codon_start=1
/protein_id="AA014420.1"
/db_xref="GI:10185736"
/translation="MSFVGENGVKMGSEDPKDEPCCLEDPAGSPLEPSPLEPTM
FVHTSRKYNLNPKKFSIHDQHKVLDVDSGLIVPKNYIRPEIFPALASLSAS
AEKGSPTLGVSKGECLYCDKDGSHPSLOLKEKELMAQKESARPEIFRYAQ
VGSNNLESAHPGWFTICSCNENPEVTDKFEKRKHIEFSFQPVCAKMSPEVSD"

BASE COUNT 246 a 196 c 190 g 185 t

ORIGIN

Query Match 88.6%; Score 512.8; DB 9; Length 817;
Best Local Similarity 99.6%; Pred. No. 4e-148;
Matches 514; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 AGAGGTCGCAAGGTGAAGAACTTAACCCGGAAGAAATTGACATTCATACAGATCAC 123
DB 214 ACAAGTCCAAAGGTGAAGAACTTAACCCGGAAGAAATTGACATTCATACAGATCAC 273

QY 124 AAAGTACTGTCCTGGAAGTCTGGAATCTCATAGCAGTTCCAGATTAATAACTATACGC 183
DB 274 AAAGTACTGTCCTGGAAGTCTGGAATCTCATAGCAGTTCCAGATTAATAACTATACGC 333

QY 184 CCAGAGATCTTCTTTCATTAAGCTTCATCTTTCATGAGCTGAGCTCTGCGAGAAAGAAAGT 243
DB 334 CCAGAGATCTTCTTTCATTAAGCTTCATCTTTCATGAGCTGAGCTCTGCGAGAAAGAAAGT 393

QY 244 CCGATTCCTCGGGGGTCTCTAAGGGGAGTTTGTCTTACTGTGACAGATTAAGA 303
DB 394 CCGATTCCTCGGGGGTCTCTAAGGGGAGTTTGTCTTACTGTGACAGATTAAGA 453

QY 304 CAAAGTCATCCATCCCTTCAGCTGAAGAGAGAAACTGATGAAGCTGGCTGCCAAAAG 363
DB 454 CAAAGTCATCCATCCCTTCAGCTGAAGAGAGAAACTGATGAAGCTGGCTGCCAAAAG 513

QY 364 GAATCAGCAGCGGGGCTTCATCTTTCATTAAGGCTCAGGTGGCTCCTGGAACATGCTG 423
DB 514 GAATCAGCAGCGGGGCTTCATCTTTCATTAAGGCTCAGGTGGCTCCTGGAACATGCTG 573

QY 424 GAGTCGGCGGCTCACCCCGGATGTTTCATCTGACCTCCTGCAATTTGAAGAGCTGTT 483
DB 574 GAGTCGGCGGCTCACCCCGGATGTTTCATCTGACCTCCTGCAATTTGAAGAGCTGTT 633

QY 484 GGGGTGACAGATTAATTGAGAACAGAAACATTTGATTTTCAACCAAGTTTGC 543
DB 634 GGGGTGACAGATTAATTGAGAACAGAAACATTTGATTTTCAACCAAGTTTGC 693

QY 544 AAAGCTGAATGAGCCCAAGTGAAGTCAAGCATTTAG 579
DB 694 AAAGCTGAATGAGCCCAAGTGAAGTCAAGCATTTAG 729

RESULT 9
AXI33934 847 bp DNA linear PAT 15-MAY-2001
LOCUS AXI33934
DEFINITION Sequence 4 from Patent EP1092773.
ACCESSION AXI33934
VERSION AXI33934.1 GI:14139876
KEYWORDS

SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 847)
AUTHORS Ushio, S., Nukada, Y., Yamamoto, K. and Kurimoto, M.
TITLE Polypeptide and uses thereof
JOURNAL Patent: EP 1092773-A 4 18-APR-2001;
KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKYUJO (JP)

FEATURES
source
1. 847
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 244 a 210 c 202 g 191 t

ORIGIN

Query Match 88.6%; Score 512.8; DB 6; Length 847;
Best Local Similarity 99.6%; Pred. No. 4.1e-148;
Matches 514; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 AGAGTCCAAAGGTGAAGAACTTAACCCGGAAGAAATTGACATTCATGACAGATCAC 123
DB 262 ACAAGTCCAAAGGTGAAGAACTTAACCCGGAAGAAATTGACATTCATGACAGATCAC 321

QY 124 AAAGTACTGTCCTGGAAGTCTGGAATCTCATAGCAGTTCCAGATTAATAACTATACGC 183
DB 322 AAAGTACTGTCCTGGAAGTCTGGAATCTCATAGCAGTTCCAGATTAATAACTATACGC 381

QY 184 CCAGAGATCTTCTTTCATTAAGCTTCATCTTTCATGAGCTGAGCTCTGCGAGAAAGAAAGT 243
DB 382 CCAGAGATCTTCTTTCATTAAGCTTCATCTTTCATGAGCTGAGCTCTGCGAGAAAGAAAGT 441

QY 244 CCGATTCCTCGGGGGTCTCTAAGGGGAGTTTGTCTTACTGTGACAGATTAAGA 303
DB 442 CCGATTCCTCGGGGGTCTCTAAGGGGAGTTTGTCTTACTGTGACAGATTAAGA 501

QY 304 CAAAGTCATCCATCCCTTCAGCTGAAGAGAGAAACTGATGAAGCTGGCTGCCAAAAG 363
DB 502 CAAAGTCATCCATCCCTTCAGCTGAAGAGAGAAACTGATGAAGCTGGCTGCCAAAAG 561

QY 364 GAATCAGCAGCGGGGCTTCATCTTTCATTAAGGCTCAGGTGGCTCCTGGAACATGCTG 423
DB 562 GAATCAGCAGCGGGGCTTCATCTTTCATTAAGGCTCAGGTGGCTCCTGGAACATGCTG 621

QY 424 GAGTCGGCGGCTCACCCCGGATGTTTCATCTGACCTCCTGCAATTTGAAGAGCTGTT 483
DB 622 GAGTCGGCGGCTCACCCCGGATGTTTCATCTGACCTCCTGCAATTTGAAGAGCTGTT 681

QY 484 GGGGTGACAGATTAATTGAGAACAGAAACATTTGATTTTCAACCAAGTTTGC 543
DB 682 GGGGTGACAGATTAATTGAGAACAGAAACATTTGATTTTCAACCAAGTTTGC 741

QY 544 AAAGCTGAATGAGCCCAAGTGAAGTCAAGCATTTAG 579
DB 742 AAAGCTGAATGAGCCCAAGTGAAGTCAAGCATTTAG 777

RESULT 10
AXI33936 855 bp DNA linear PAT 15-MAY-2001
LOCUS AXI33936
DEFINITION Sequence 6 from Patent EP1092773.
ACCESSION AXI33936
VERSION AXI33936.1 GI:14139877
KEYWORDS human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 855)
AUTHORS Ushio, S., Nukada, Y., Yamamoto, K. and Kurimoto, M.
TITLE Polypeptide and uses thereof
JOURNAL Patent: EP 1092773-A 6 18-APR-2001;
KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKYUJO (JP)

BASE COUNT 214 a 190 c 172 g 178 t
 ORIGIN

Query Match 87.0%; Score 504; DB 6; Length 754;
 Best Local Similarity 100.0%; Pred. NO. 2.2e-145;
 Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 GTGAGAACTTAACCCGGAAGAAATTCAGCATTCACACAGATCAGCAAAAGTACTGGTC 135
 DB 181 GTGAGAACTTAACCCGGAAGAAATTCAGCATTCACACAGATCAGCAAAAGTACTGGTC 240
 QY 136 CTGGACTCTGGGAATCTCTACAGTTCACATTAATAAATCTACATACGCCAGATCTTC 195
 DB 241 CTGGACTCTGGGAATCTCTACAGTTCACATTAATAAATCTACATACGCCAGATCTTC 300
 QY 196 TTTCATAGCTCATCTTGTAGCTCAGCCTCTGGGAGAAAGAAAGTCCGATTCCTCG 255
 DB 301 TTTCATAGCTCATCTTGTAGCTCAGCCTCTGGGAGAAAGAAAGTCCGATTCCTCG 360
 QY 256 GGGGTCTTAAGGGAGTTTGTCTACTGTGACAAAGATTAAGGACAAAGTCATCCA 315
 DB 361 GGGGTCTTAAGGGAGTTTGTCTACTGTGACAAAGATTAAGGACAAAGTCATCCA 420
 QY 316 TCCCTTACCTGAAGAGAAAGAACTGATGAGTGGCTGCCCAAAAGAAATCAGCAGC 375
 DB 421 TCCCTTACCTGAAGAGAAAGAACTGATGAGTGGCTGCCCAAAAGAAATCAGCAGC 480
 QY 376 CGGCTTCATCTTTATATAGGGCTCAGTGGCTCCTGGAAATCTGGAGTGGGCT 435
 DB 481 CGGCTTCATCTTTATATAGGGCTCAGTGGCTCCTGGAAATCTGGAGTGGGCT 540
 QY 436 CACCCCGGATGTTTATCTGCACCTCTGCAATTTGTAATGAGCTGTGGGGTGACAT 495
 DB 541 CACCCCGGATGTTTATCTGCACCTCTGCAATTTGTAATGAGCTGTGGGGTGACAT 600
 QY 496 AATTTGAGACAGAAACAACTGATGATTTTCAATTCACCAAGTTGCAAGCTGAATG 555
 DB 601 AATTTGAGACAGAAACAACTGATGATTTTCAATTCACCAAGTTGCAAGCTGAATG 660
 QY 556 AGCCCACTGAGTGCAGCGATTAG 579
 DB 661 AGCCCACTGAGTGCAGCGATTAG 684

RESULT 13
 AF251120 537 bp mRNA linear PRI 03-MAY-2001
 LOCUS
 DEFINITION Homo sapiens interleukin-1-related protein short isoform mRNA,
 complete cds; alternatively spliced.
 ACCESSION AF251120
 VERSION AF251120.1 GI:10185739
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS 1 (bases 1 to 537)
 Pan, G., Risse, P., Mao, W., Baldwin, D.T., Zhong, A.W., Filvaroff, E.,
 Yansura, D., Lewis, L., Eigenbrodt, C., Henzel, W.J., and Vanden, R.
 IL-1H, an interleukin 1-related protein that binds IL-18
 receptor/IL-1Rrp
 TITLE Cytokine 13 (1), 1-7 (2001)
 JOURNAL
 MEDLINE 21066552
 PUBMED 11145836
 REFERENCE 2 (bases 1 to 537)
 Pan, G., Baldwin, D.T., and Zhong, A.W.
 TITLE Direct Submission
 JOURNAL Submitted (03-APR-2000) Endocrinology, Genentech, Inc., 1 DNA Way,
 South San Francisco, CA 94080, USA
 FEATURES
 source 1..537
 Location/Qualifiers
 /organism="Homo sapiens"

CDS
 /db_xref="taxon:9606"
 1..537

/note="IL-1H; IL-1 family member; binds IL-18
 receptor/IL-1Rrp; putative involvement in inflammation and
 immune responses"

/codon_start=1
 /product="interleukin-1-related protein short isoform"
 /protein_id="AF014422.1"
 /db_xref="GI:10185740"
 /translation="MSFVGENSGVKMSSEDEMERPOCCLEDPAYSPLEPGSLPAM
 FVHTKIFPLASLSASAEKSPILIGKSEFCLCYCKDGSHPSIQKKEKLMK
 LAOKESARPRFVRAOYGSNNMLESAAHPMFICTSCNCEPVGVIDKPFNRKHIE
 FSRPVCRAEMSEVSD"

BASE COUNT 141 a 129 c 142 g 125 t
 ORIGIN

Query Match 68.5%; Score 396.6; DB 9; Length 537;
 Best Local Similarity 96.7%; Pred. No. 5.4e-112;
 Matches 405; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 161 TTCAGATAAATACTATACAGCCAGATCTCTTGTGATTAAGCTCCTAGACT 220
 DB 119 TCCCGCATGAATTTGTTACACAAAGATCTTGTGATTAAGCTCCTAGACT 178
 QY 221 CAGCTCTGGGAGAAAGAAAGTCCATCTCTGGGGGTCTTAAAGGAGATTTTTC 280
 DB 179 CAGCTCTGGGAGAAAGAAAGTCCATCTCTGGGGGTCTTAAAGGAGATTTTTC 238
 QY 281 TCTACTGTGACAAAGATTAAGGAAAGTATCATCATCTCTTCACTGTAAGAGAAAC 340
 DB 239 TCTACTGTGACAAAGATTAAGGAAAGTATCATCATCTCTTCACTGTAAGAGAAAC 298
 QY 341 TGATGAAGTGGCTGCCCAAAAGAAAGTATCATCATCTCTTCACTGTAAGAGCTC 400
 DB 299 TGATGAAGTGGCTGCCCAAAAGAAAGTATCATCATCTCTTCACTGTAAGAGCTC 358
 QY 401 AGGAGGCTCTCTGGAATCATCTGAGTGGGGCTCACCCGGATGGTTCATCTGACCT 460
 DB 359 AGGAGGCTCTCTGGAATCATCTGAGTGGGGCTCACCCGGATGGTTCATCTGACCT 418
 QY 461 CCTGCAATTTGTAAGAGCTGTGGGGTGACAGATAATTTGAGAAACAGAAACATTG 520
 DB 419 CCTGCAATTTGTAAGAGCTGTGGGGTGACAGATAATTTGAGAAACAGAAACATTG 478
 QY 521 AATTTTCAATTTCAACCAAGTTTGCAGAGCTGAATGAGCCCACTGAGGATTAG 579
 DB 479 AATTTTCAATTTCAACCAAGTTTGCAGAGCTGAATGAGCCCACTGAGGATTAG 537

RESULT 14
 AY071841 474 bp mRNA linear PRI 20-MAY-2002
 LOCUS
 DEFINITION Homo sapiens IL-1E7e (IL1E7) mRNA, complete cds, alternatively
 spliced.
 ACCESSION AY071841
 VERSION AY071841.1 GI:19068185
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS 1 (bases 1 to 474)
 Taylor, S.L., Renshaw, B.R., Garza, K.E., Smith, D.E. and Sims, J.E.
 TITLE Genomic organization of the interleukin-1 locus
 JOURNAL Genomics 79 (5), 726-733 (2002)
 MEDLINE 11991723
 PUBMED 11991723
 REFERENCE 2 (bases 1 to 474)
 Taylor, S.L., Renshaw, B.R., Garza, K.E., Smith, D.E. and Sims, J.E.
 TITLE Direct Submission
 JOURNAL Submitted (26-DEC-2001) Molecular Genetics, Immunex Corporation, 51
 University Street, Seattle, WA 98101, USA
 FEATURES
 Location/Qualifiers

```
source 1..474
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /chromosome="2"
        /map="2q"
gene 1..474
      /gene="IL1F7"
      /gene="IL1F7"
      /note="cytokine; alternatively spliced"
      /product="IL-1F7e"
      /protein_id="AAL67154.1"
      /db_xref="GI:19068186"
      /translation="MSFVGENSGVKMSDEMDPEQCELEIFEFALASLSASAQK
      GSPILVSGSERFLCDKDGSHSLDKKKLKKLAKQESARPRPTFPAQVGS
      MNMLESAHGHMCTCTSCNCPNPEVYTDKFNKKHIEFSFQVCKAEMSPSEVSD"
BASE COUNT 126 a 104 c 130 g 114 t
ORIGIN
Query Match 68.0%; Score 394; DB 9; Length 474;
Best Local Similarity 100.0%; Pred. No. 3.4e-111;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 186 AGAGATCTCTTTGCAATTAAGGAGGAGTTTGTCTCTACTGTGACAGATTAAGGACA 245
    |||||||
Db 81 AGAGATCTCTTTGCAATTAAGGAGGAGTTTGTCTCTACTGTGACAGATTAAGGACA 140
QY 246 GATTCTCTGGGGGTCTCTAAAGGGAGTTTGTCTCTACTGTGACAGATTAAGGACA 305
    |||||||
Db 141 GATTCTCTGGGGGTCTCTAAAGGGAGTTTGTCTCTACTGTGACAGATTAAGGACA 200
QY 306 AAGTCATCATCCCTTCACTGAGTGAAGAGAACTGATGAAGCTGCGCCCAAAAGGA 365
    |||||||
Db 201 AAGTCATCATCCCTTCACTGAGTGAAGAGAACTGATGAAGCTGCGCCCAAAAGGA 260
QY 366 ATCAGCAGCGCGGCTTCATCTTTATAGGGCTCAGGTGGGCTCTGCAACATGCTGGA 425
    |||||||
Db 261 ATCAGCAGCGCGGCTTCATCTTTATAGGGCTCAGGTGGGCTCTGCAACATGCTGGA 320
QY 426 GTGGGGGGCTCACCGCGGATGTTTCATCTGCACTCTGCAATTTGATAGCGCTGTGG 485
    |||||||
Db 321 GTGGGGGGCTCACCGCGGATGTTTCATCTGCACTCTGCAATTTGATAGCGCTGTGG 380
QY 486 GGTGACAGATTAATTTGAGAAACAGAAACATTTGATTTCAATTCACAGTTTGCAA 545
    |||||||
Db 381 GGTGACAGATTAATTTGAGAAACAGAAACATTTGATTTCAATTCACAGTTTGCAA 440
QY 546 AGCTGAATAGAGCCCACTGAGGTGAGCGATTAG 579
    |||||||
Db 441 AGCTGAATAGAGCCCACTGAGGTGAGCGATTAG 474

RESULT 15
AXI33932 575 bp DNA linear PAT 15-MAY-2001
LOCUS AXI33932
DEFINITION Sequence 2 from Patent EP1092773.
ACCESSION AXI33932
VERSION AXI33932.1 GI:14139874
KEYWORDS
SOURCE unidentfied.
        ORGANISM unidentfied.
        unclassified.
REFERENCE 1 (bases 1 to 575)
AUTHORS Ushio,S., Nukada,Y., Yamamoto,K. and Kurimoto,M.
TITLE Polypeptide and uses thereof
JOURNAL Patent: EP 1092773-A 2 18-APR-2001;
        KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKYUJO (JPN)
FEATURES
        source
        1..575
        /organism="unidentfied"
        /db_xref="taxon:32644"
BASE COUNT 172 a 142 c 141 g 120 t
```

```
ORIGIN
Query Match 53.7%; Score 310.8; DB 6; Length 575;
Best Local Similarity 99.4%; Pred. No. 2.7e-85;
Matches 312; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 64 AGAGTCCAAAGGTGAAGAACTTAAACCGAAGAAATTCAGATTCATGACCGAGATGAC 123
    |||||||
Db 262 ACAAGTCCAAAGGTGAAGAACTTAAACCGAAGAAATTCAGATTCATGACCGAGATGAC 321
QY 124 AAAGTACTGATCCTGAGCTCTGGGAATTCATAGCAGTTCCAGATTAATAACTATACGAC 183
    |||||||
Db 322 AAAGTACTGATCCTGAGCTCTGGGAATTCATAGCAGTTCCAGATTAATAACTATACGAC 381
QY 184 CCAAGATCTCTTTGCAATTAAGCTTCATCTTGTAGCTAGGCTGCGGAGAAAGAAAGT 243
    |||||||
Db 382 CCAAGATCTCTTTGCAATTAAGCTTCATCTTGTAGCTAGGCTGCGGAGAAAGAAAGT 441
QY 244 CCGATCTCTGAGGGGTCTCTAAAGGGAGTTTGTCTCTACTGTGACAGGATTAAGGA 303
    |||||||
Db 442 CCGATCTCTGAGGGGTCTCTAAAGGGAGTTTGTCTCTACTGTGACAGGATTAAGGA 501
QY 304 CAAAGTCATCATCCCTTCACTGAGTGAAGAGAAACATGATAGCTGCGCCCAAAAG 363
    |||||||
Db 502 CAAAGTCATCATCCCTTCACTGAGTGAAGAGAAACATGATAGCTGCGCCCAAAAG 561
QY 364 GAATCAGCAGCGCG 377
    |||||||
Db 562 GAATCAGCAGCGCG 575
```

Search completed: May 3, 2003, 06:02:45
Job time : 1803 sec

GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 3, 2003, 02:24:11 ; Search time 228 Seconds
(without alignments)
5718.890 Million cell updates/sec

Title: US-09-876-790-1

Perfect score: 579
1 atgcagcgtctgtatagagag.....ccagtgagtcagcgcattag 579

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	579	100.0	579	21	AAA27918
2	517.8	89.4	594	21	AAA27921
3	516	89.1	650	21	AAA51592
4	516	89.1	1006	21	AAA51591
5	512.8	88.6	657	21	AAA27920
6	512.8	88.6	657	21	AAA08513
7	512.8	88.6	802	21	AAC66727
8	512.8	88.6	802	22	AAAF84120
9	512.8	88.6	839	21	AAA51604

10	512.8	88.6	847	22	AAAC85680
11	512.8	88.6	1104	22	AAAT71179
12	512.8	88.6	1600	21	AAAD00210
13	511.8	88.4	626	21	AAA51601
14	510.8	88.2	657	21	AAAD00212
15	509.6	88.0	630	22	AAAC84317
16	506.4	87.5	1225	21	AAA08512
17	504	87.0	754	21	AAA51593
18	504	87.0	754	22	AAAF92128
19	497.6	85.9	629	21	AAA51594
20	492	85.0	561	21	AAA51603
21	395.6	68.3	506	21	AAA51602
22	394	68.0	474	21	AAA27922
23	394	68.0	636	21	AAAD00214
24	393.6	68.0	989	20	AAAX22308
25	390.6	67.5	408	20	AAAX22311
26	390.6	67.5	501	20	AAAX22310
27	390.6	67.5	534	20	AAAX22309
28	367.4	63.5	654	21	AAAD00213
29	365.8	63.2	654	21	AAAD00214
30	281	48.5	471	21	AAAD00215
31	279.4	48.3	471	21	AAAD00216
32	273	47.2	371	22	AAAB84375
33	251	43.4	1471	20	AAZ066633
34	251	43.4	28866	20	AAAX22304
35	122	21.1	140	22	AAAT71180
36	120	20.7	120	22	AAAT71178
37	51.2	8.8	1073	22	AAAD12296
38	51.2	8.8	1183	19	AAAV42659
39	51.2	8.8	1183	20	AAAX90135
40	51.2	8.8	1183	22	AAAS26842
41	51.2	8.8	1291	20	AAAX86458
42	51.2	8.8	1377	20	AAAX86459
43	50.6	8.7	673	22	AAAD16762
44	50.6	8.7	673	22	AAAD16762
45	48.6	8.4	520	22	AAAF83869

ALIGNMENTS

RESULT 1
AAA27918
ID AAA27918 standard; cDNA; 579 BP.
XX
AC AAA27918:
XX
DT 12-SEP-2000 (first entry)
XX
DE Human interleukin-1 zeta cDNA coding region.
XX
KW Interleukin-1 zeta; IL-1 zeta; human; chromosome 2; gene therapy;
KW glaucoma; ectodermal dysplasia; wrinkly skin syndrome;
KW insulin-dependent diabetes mellitus; leukaemia; lymphoma;
KW tibial muscular dystrophy; ss.
OS Homo sapiens.
XX
PN WO200036108-A2.
XX
PD 22-JUN-2000.
XX
PF 14-DEC-1999; 99WO-US29549.
XX
PR 14-DEC-1998; 98US-0112163.
XX
PR 10-NOV-1999; 99US-0164675.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Sims JE, Smith DE, Born TL;
XX
DR WPI: 2000-442387/38.
DR P-PSDB; AAY95297.

cDNA encoding IL-1
Human interleukin
Human zll144 cDNA.
Human IL-1 recepto
Human IL-1 recepto
Human EXOS encodin
Human interleukin
Processed human IL
Human PRO3435 cDNA
Human IL-1 recepto
Human IL-1 recepto
Human IL-1 recepto
Human interleukin-
Human zll144 splic
Human Tango-77 cDN
Human Tango-77 cDN
Human Tango-77 cDN
Human Tango-77 cDN
Human zll144 degen
Human zll144-E200K
Degenerate cDNA-1
Degenerate cDNA-2
Human polynucleoti
Portion of Tango-7
Human IL-1ra BAC c
Human interleukin
Human interleukin
Human interleukin-
cDNA encoding inte
Human interleukin-
Human cDNA encodin
cDNA encoding a hu
cDNA encoding a hu
Human cDNA encodin
Human novel protei
Human interleukin-

xx Isolated interleukin-1 (IL-1) zeta nucleic acids and splice variants
 pt TDD1, TDD2, TDD3 and their encoding proteins, useful as probes for
 pt identifying genes associated with diseases such as glaucoma, and
 pt insulin-dependent diabetes mellitus -
 xx Claim 1(a); Page 8, 87pp: English.

The present sequence is that of the coding region of cDNA encoding human interleukin-1 zeta (IL-1 zeta, see AAV95297), a member of the IL-1 family. The sequence was deduced from EST IMAGE clone 152871, which encodes a partial open reading frame, and from additional sequences obtained from PCR and 5' RACE reactions. IL-1 zeta mRNA is expressed most strongly in the testis, prostate, colon, brain, placenta, lung, foetal liver and lymph node. The invention is directed to novel, purified and isolated IL-1 zeta, IL-1 zeta splice variants and Xrac2 polypeptides (see AAV95297-301), the nucleic acids (see AAV7918-22) encoding such polypeptides, processes for production of recombinant forms of such polypeptides, and their uses. IL-1 zeta nucleic acids are used to: to express IL-1 zeta polypeptides; as probes to identify nucleic acids encoding members of the IL-1 ligand family; to identify human chromosome 2; to map genes on chromosome 2; to identify genes associated with diseases, syndromes, or other conditions associated with chromosome 2, such as glaucoma, ectodermal dysplasia, insulin-dependent diabetes mellitus, wrinkly skin syndrome, T-cell leukaemia or lymphoma, and tibial muscular dystrophy; as single-stranded sense or antisense oligonucleotides to inhibit expression of IL-1 zeta polypeptides; to help detect defective genes in an individual; and for gene therapy.

SQ Sequence 579 BP; 173 A; 129 C; 146 G; 131 T; 0 other;

Query Match	100.0%;	Score 579;	DB 21;	Length 579;
-------------	---------	------------	--------	-------------

Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATATCAGGCTGTGATAGAGAGGAAACGAAACCAAGGAAAGAACAGCTTTAAAGACGC	60
Db	1	ATATCAGGCTGTGATAGAGAGGAAACGAAACCAAGGAAAGAACAGCTTTAAAGACGC	60
QY	61	TTAAGAGGTCCAAAGGTGAAGACTTAAACCCGAGAAGAAATTCAGCATTCATGACCAGGAT	120
Db	61	TTAAGAGGTCCAAAGGTGAAGACTTAAACCCGAGAAGAAATTCAGCATTCATGACCAGGAT	120
QY	121	CACAAGATCTGAGTCCCTGAGCTGGGAATCTATATGACATTCAGATTCAGATTAATACTAATA	180
Db	121	CACAAGATCTGAGTCCCTGAGCTGGGAATCTATATGACATTCAGATTCAGATTAATACTAATA	180
QY	181	CGCCGAGAGATCTTCTTTGCAATTAGCCTCATCCTTGAAGCTCAGCCTCGCGAGAAAGGA	240
Db	181	CGCCGAGAGATCTTCTTTGCAATTAGCCTCATCCTTGAAGCTCAGCCTCGCGAGAAAGGA	240
QY	241	AGTCGATTCCTCTGAGGGGGTCCTAAAGGGGAGCTTTGTCCTACTGTGAAAGATAA	300
Db	241	AGTCGATTCCTCTGAGGGGGTCCTAAAGGGGAGCTTTGTCCTACTGTGAAAGATAA	300
QY	301	GGACAAAGTCATCCATCCCTTCAGCTGAGAAAGAGAGAAATCATCAACCTGGTGGCCAA	360
Db	301	GGACAAAGTCATCCATCCCTTCAGCTGAGAAAGAGAGAAATCATCAACCTGGTGGCCAA	360
QY	361	AAGGATTCAGCAGCGCGGCGCTTCATCTTTATAGGGCTCAGTGGGCTCCTGGAAATG	420
Db	361	AAGGATTCAGCAGCGCGGCGCTTCATCTTTATAGGGCTCAGTGGGCTCCTGGAAATG	420
QY	421	CTTGAGTCTGGCGGCTCACCCCGGATGGTTCATTCGACCTCCTGCAATTTGAATGAGCCT	480
Db	421	CTTGAGTCTGGCGGCTCACCCCGGATGGTTCATTCGACCTCCTGCAATTTGAATGAGCCT	480
QY	481	GTTCGGGTACAGATTAATTTGAGAACAGGAAACATATGATTTTCATTTCAACCAAGTT	540
Db	481	GTTCGGGTACAGATTAATTTGAGAACAGGAAACATATGATTTTCATTTCAACCAAGTT	540

[illegible]

RESULT 2	
AAA27921	
ID	AAA27921 standard; cDNA; 594 BP
vv	

DT	12-SEP-2000 (first entry)
XX	
DE	Human interleukin-1 zeta splice variant TD2.2 cDNA

Homo sapiens

PN WO200036108-A2.

PD 22-JUN-2000

PF 14-DEC-1999; 99WO-US29549.

PR 14-DEC-1998; 98US-0112163.

XX

PA (IMMV) IMMUNEX CORP.

PI Sims JE, Smith DE, Born TL;

DR WPI; 2000-442387/38

XX

PT Isolated interleukin-1 (IL-1) zeta nucleic acids and splice variants
PT TD21, TD22, and their encoding proteins, useful as probes for
PT identifying genes associated with diseases such as glaucoma, and
PT insulin-dependent diabetes mellitus -
XX
PS Claim 1(a); Page 10; 87pp; English.

The present sequence is that of the coding region of cDNA encoding splice variant TDZ.2 (testis-derived zeta variant, see AA95300) of human interleukin-1 zeta (IL-1 zeta). TDZ.2 mRNA is generated from exons 1, 4, 5 and 6 of the IL-1 zeta locus on chromosome 2, and the encoded protein is probably a functional IL-1 like molecule. TDZ.2 mRNA is expressed most strongly in the testis and bone marrow. The invention is directed to novel, purified and isolated IL-1 zeta, its splice variants and Xrec2 polypeptides (see AA95297-301), the nucleic acids (see AA92918-2) encoding such polypeptides, processes for production of recombinant forms of such polypeptides, and their uses. TDZ.2 nucleic acids are used to: to express TDZ.2 polypeptides; as probes to identify nucleic acids encoding proteins of the IL-1 ligand family; to identify human chromosome 2; to map genes on chromosome 2; to identify genes associated with diseases, syndromes, or other conditions associated with chromosome 2, such as glaucoma, ectodermal dysplasia, insulin-dependent diabetes mellitus, writhly skin syndrome, T-cell leukemia or lymphoma, and tibial muscular dystrophy; as single-stranded sense or antisense oligonucleotides to inhibit expression of TDZ.2 polypeptides; to help detect defective genes in an individual; and for gene therapy.

594 Sequence 594 BP; 169 A; 133 C; 154 G; 138 T; 0 other;

Query Match	89.48;	Score 517.8;	DB 21;	Length 594;
Best Local Similarity	99.68;	Pred. No. 8.5e-163;		
Matches 519; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0


```
DB 526 GGGGTGACAGATTAATTGGAGACAGGAACACATTGATTTTCATTTCAACCGATTGC 585
QY 544 AAAGCTGAATGAGCCCCAGTCAGTCAGCATTAG 579
DB 586 AAAGCTGAATGAGCCCCAGTCAGTCAGCATTAG 621

RESULT 4
AAA51591
ID AAA51591 standard; DNA; 1006 BP.
XX
AC AAA51591;
XX
DE 31-OCT-2000 (first entry)
XX
KW Human IL-1 receptor antagonist 1 related DNA.
XX
KW hIL-1Ra1; human interleukin-1 receptor antagonist-1; IL-1Ip; osteopathic;
KW interleukin-1-like polypeptide; anti-inflammatory; anti-asthmatic;
KW anti-arthritis; antimicrobial; respiratory; anti-ischemic; vaccine;
KW dermatological; immunomodulatory; gastrointestinal; gene therapy; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 103..936
FT FT /*tag= a
FT FT 103..180
FT FT /*tag= b
FT FT 180..432
FT FT /*tag= c
FT FT 433..933
FT FT /*tag= d
XX
PN MO200039297-A2.
XX
PD 06-JUL-2000.
XX
PF 22-DEC-1999; 99WO-US30720.
XX
PR 23-DEC-1998; 98US-0113430.
PR 22-JAN-1999; 98US-0116843.
PR 13-APR-1999; 99US-0129122.
XX
PA (GETH ) GENENTECH INC.
XX
PI Goddard A, Pan J;
XX
DR WPI: 2000-452395/39.
XX P-PSDB: AAY96931, AAY96932.
XX
PT Nucleic acids encoding interleukin-1-like polypeptides, useful for
PT preventing and treating e.g. inflammation, asthma and psoriasis
XX
XX Example 1; Fig 1A-B; 143pp; English.
XX
CC An isolated nucleic acid molecule encoding an interleukin-1-like
CC polypeptide (IL-1Ip) that retains one or more activities of the peptide
CC from which it is derived, such as the IL-18R binding activity of a human
CC interleukin-1 receptor antagonist-1 (hIL-1Ra1) polypeptide, is new. The
CC nucleic acids may be used in molecular engineering applications, e.g.
CC hybridization assays and chromosome and gene mapping studies, for
CC recombinantly producing the IL-1Ip polypeptide or for producing gene
CC knock out animals to study the role of the protein in metabolism and
CC disease processes (conversely, gene therapy protocols may be used to
CC supplement a patient's production of the polypeptide or to rectify
CC mutations that lead to the production of in active peptides). The
CC peptides produced may be used to screen for and produce modulators (e.g.
CC antibodies) of IL-1Ip protein expression and activity which may be use
CC to treat disorders associated with inappropriate IL-1Ip expression and
CC activity, such as inflammatory disorders, asthma, arthritis,
CC osteoarthritis, sepsis, acute lung injury, adult respiratory distress
```

```
CC syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
CC psoriasis, graft versus host disease and/or inflammatory bowel disease.
XX
SQ Sequence 1006 BP; 289 A; 246 C; 241 G; 230 T; 0 other;
Query Match 89.1%; Score 516; DB 21; Length 1006;
Best Local Similarity 100.0%; Pred. No. 4,6e-162;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 64 AGAGTCCAAAGGTAAGACTTAAACCCGAGAAATTCACATTCATGACCAGATCAC 123
DB 421 AGAGTCCAAAGGTAAGACTTAAACCCGAGAAATTCACATTCATGACCAGATCAC 480
QY 124 AAAGTACTGTCCTGAGCTGGGAATCTCATAGAGTTCAGAPAAAATACATACGCC 183
DB 481 AAAGTACTGTCCTGAGCTGGGAATCTCATAGAGTTCAGAPAAAATACATACGCC 540
QY 184 CCAGAGATCTTCTTGTGATAGCCTCATCTTGAGCTCAGCCTCGGAGAGAAAGAGT 243
DB 541 CCAGAGATCTTCTTGTGATAGCCTCATCTTGAGCTCAGCCTCGGAGAGAAAGAGT 600
QY 244 CCGATTCTCTGGGGGCTCTTAAGGGAGTTTGTCTCTACTGTACAAAGATAAAGA 303
DB 601 CCGATTCTCTGGGGGCTCTTAAGGGAGTTTGTCTCTACTGTACAAAGATAAAGA 660
QY 304 CAAAGTCAATCCATCCCTTCACCTGAGAGAGAGAAAGATGAGAGTGGCCCAAAAG 363
DB 661 CAAAGTCAATCCATCCCTTCACCTGAGAGAGAGAAAGATGAGAGTGGCCCAAAAG 720
QY 364 GAATCAGCAGCCCGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCCTGGAAACATCTG 423
DB 721 GAATCAGCAGCCCGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCCTGGAAACATCTG 780
QY 424 GAGTCGGGGCTCACCCCGGATGTTGATCTGCACTTCGACCTTCGATTTGATGACCTGT 483
DB 781 GAGTCGGGGCTCACCCCGGATGTTGATCTGCACTTCGACCTTCGATTTGATGACCTGT 840
QY 484 GGGGTGACAGATTAATTGAGAACAGAAACACATTAATTTTCATTTCAACCGATTGC 543
DB 841 GGGGTGACAGATTAATTGAGAACAGAAACACATTAATTTTCATTTCAACCGATTGC 900
QY 544 AAAGCTGAATGAGCCCCAGTCAGTCAGCATTAG 579
DB 901 AAAGCTGAATGAGCCCCAGTCAGTCAGCATTAG 936

RESULT 5
AAA27920
ID AAA27920 standard; cDNA; 657 BP.
XX
AC AAA27920;
XX
DE 12-SEP-2000 (first entry)
XX
KW Human interleukin-1 zeta splice variant TDZ.1 cDNA.
XX
OS Homo sapiens.
XX
PN WO200036108-A2.
XX
PD 22-JUN-2000.
XX
PF 14-DEC-1999; 99WO-US29549.
XX
PR 14-DEC-1998; 98US-0112163.
PR 10-NOV-1999; 99US-0164675.
XX
PA (IMMUNEX ) IMMUNEX CORP.
```


XX Sims JE, Smith DE, Born TL;
PI
XX
XX WPI: 2000-442387/38.
DR
DR p-PSDB; AAY95299.
XX
XX Isolated interleukin-1 (IL-1) zeta nucleic acids and splice variants-
PT
PT TDD1, TDD2, TDD3 and their encoding proteins, useful as probes for
PT identifying genes associated with diseases such as glaucoma, and
PT insulin-dependent diabetes mellitus -
XX
XX Claim 1(a); Page 9-10; 87pp; English.

CC The present sequence is that of the coding region of cDNA encoding
CC splice variant TD2.1 (testis-derived zeta variant, see AA95299) of
CC human interleukin-1 zeta (IL-1 zeta). TD2.1 mRNA is generated from
CC exons 1, 2, 4, 5 and 6 of the IL-1 zeta locus on chromosome 2, and
CC the encoded protein is probably a functional IL-1 like molecule.
CC TD2.1 mRNA is expressed most strongly in the kidney, skeletal
CC muscle, testis, prostate, ovary, colon, small intestine, liver,
CC placenta, lung, tonsil, foetal liver, lymph node and bone marrow.
CC The invention is directed to novel, purified and isolated IL-1
CC zeta, its splice variants and Xrc2 polypeptides (see AA95297-301),
CC the nucleic acids (see AA27918-22) encoding such polypeptides,
CC processes for production of recombinant forms of such polypeptides,
CC and their uses. TD2.1 nucleic acids are used to: to express TD2.1
CC polypeptides; as probes to identify nucleic acids encoding
CC proteins of the IL-1 ligand family; to identify human chromosome 2;
CC to map genes on chromosome 2; to identify genes associated with
CC diseases, syndromes, or other conditions associated with chromosome
CC 2, such as glaucoma, ectodermal dysplasia, insulin-dependent
CC diabetes mellitus, wrinkly skin syndrome, T-cell leukaemia or
CC lymphoma, and tibial muscular dystrophy; as single-stranded sense
CC or antisense oligonucleotides to inhibit expression of TD2.1
CC polypeptides; to help detect defective genes in an individual; and
CC for gene therapy.

SQ Sequence 657 BP; 185 A; 158 C; 165 G; 149 T; 0 other;

Query Match	88.6%;	Score 512.8;	DB 21;	Length 657;
Best Local Similarity	99.6%;	Pred. NO. 4.3e-161;		

Matches 514; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	64	AGAGTCCAAAGGAGGAGAACTTAAACCCGAAAGAAATTCAGCATTCATGACCGAGATCAC	123
Dp	142	ACAAAGTCCAAAGGAGGAGAACTTAAACCCGAAAGAAATTCAGCATTCATGACCGAGATCAC	201
QY	124	AAAGTACGAGCTGAGACTGCGGAACTCATAGCACTTCACAGTAAAACTCATACGC	183
Dp	202	AAAGTACTGGCTCGGACTCTGGGAACTCATAGCACTTCACAGTAAAACTCATACGC	261
QY	184	CCAGAGATCTTCTTTGCATTAGCCTCATCCCTTGAGCTCAGCCTCTCGGAGAAAGAACT	243
Dp	262	CCAGAGATCTTCTTTGCATTAGCCTCATCCCTTGAGCTCAGCCTCTCGGAGAAAGAACT	321
QY	244	CCGATTCCTCTGGGGGCTCTAAAGGGAGATTTGTCTACTGTGACAAAGATTAAAGA	303
Dp	322	CCGATTCCTCTGGGGGCTCTAAAGGGAGATTTGTCTACTGTGACAAAGATTAAAGA	381
QY	304	CAAGTCATCCATCCCTTCAGCTAABAAGAGAAACTGATGAAGCTGCTGCCAAAG	363
Dp	382	CAAAAGTCATCCATCCCTTCAGCTAABAAGAGAAACTGATGAAGCTGCTGCCCAAAAG	441
QY	364	GAATCAGACAGCCCGGCCCTTCATTTTATAGGGCTAGGTGGGCTCCGGAACAATGCTG	423
Dp	442	GAATCAGACAGCCCGGCCCTTCATTTTATAGGGCTAGGTGGGCTCCGGAACAATGCTG	501
QY	424	GAGTCGGGCGCTCAACCCCGAGTGTTCATCTGCACCTCTGCACATTTGATGAGCCTGTT	483
Dp	502	GAGTCGGGCGCTCAACCCCGAGTGTTCATCTGCACCTCTGCACATTTGATGAGCCTGTT	561
QY	484	GGGCTGACAGTAAATTTGAGACAGAAACACATTGAATTTTCATTCACCAAGTTTGC	543

Db 562 GGGGTACAGATTAATTTTGAGAACAGGAACACATTGAATTTTCATTTCACCAATTGC 621

QY 544 AAAGCTGAATAGCCCCAGTAGGTACGCAATTAG 579

622 AAAGCTGAATAGCCCCAGTAGGTACGCAATTAG 657

RESULT 6	
AAA08513	
ID	AAA08513 standard; DNA; 657 BP.

XX 10 TH 2000

DI 19-JUL-2000 (11st entry,
XX

Primate interleukin-1 like (IL-1-zeta) alternative coding sequence

XX

Primate; interleukin-1 like; IL-1-zeta; systemic inflammation; fever;

KW hypoglycemia; plasma

Plasma col

OS Mammalia.

XX

PN W0200017363-
yy

AA
PD 30-MAR-2000XX
9
7
6
5
4
3
2
1

PF 17-SEP-1999; 99WO-US20868

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

PR 18-SEP-1998; 9805-01
XX

PA (SCHE) SCHERING CORP.

XX

Timans JC;

XX
WPB : 2000-282599/24

DR WFL, 2000 283386/
DR P-PSDB: AAY91885

XX
v
c
o
n
t
e
n
t
s

PT New mammalian interleukin 1 like molecule, designated IL-1-zeta, useful

PT for diagnostic and therapeutic purposes, comprises a 128 amino acid

P1 sequence

PS Disclosure: Page 102-103: 110bp; English.

The present sequence encodes a primate interleukin-1 like molecule, designated IL-1-zeta. It is an alternative sequence to AAA08512, CC perhaps an allelic variant. The specification claims an isolated or CC recombinant polypeptide that: (a) specifically binds polyclonal CC antibodies generated against at least a 12 consecutive amino acid segment CC of IL-1-zeta (see AA91984) or its allelic variant (see AA91855); and CC (b) comprises at least one sequence selected from: AA91886-903 or CC AA91904-06. The preferred 12 consecutive amino acid segment is chosen CC from AA91907-18 or AA91919-21. IL-1-zeta is likely to play a role in CC systemic inflammatory reactions, such as fever, hypoglycemia, reduced CC plasma iron and zinc, the acute response of the liver, and increase CC plasma copper. IL-1-zeta binding compounds (comprising antigen binding CC sites) and IL-1-zeta polypeptides are also useful for both diagnostic and CC therapeutic purposes.

Sequence 657 BP; 184 A; 158 C; 166 G; 149 T; 0 other;

Query Match	88.6%; Score 512.8; DB 21; Length 657
Best Local Similarity	90.6%; Score 512.8; DB 21; Length 657
Best Local Alignment	90.6%; Score 512.8; DB 21; Length 657

best local similarity: 99.0%; Freq. NO. 4.3e101;
Matches 514; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY	64	AGAGGGCTCAAGGATGAAAGAACTTAAACCCGAAGAATAATTAGCATTCATGACCAGATCAC	133
Dd	142	ACAAAGTCAAAGGTGAAGAACTTAAACCCGAAGAATAATTAGCATTCATGACCAGATCAC	201
OY	124	AAAAGTACTGATCGTCTTGAGACTCTGGGAATCTTCATATGACAGTGCAGATAAAACTATCATCGC	183
Dd	202	AAAAGTACTGATCGTCTTGAGACTCTGGGAATCTTCATATGACAGTGCAGATAAAACTATCATCGC	261

QY 184 CCAGAGATCTTCTTGGCATTAGCCTCATCTGAGCTCAGCCCTCTCGGAGAAAGAGT 243
 |||||
 Db 262 CCAGAGATCTTCTTGGCATTAGCCTCATCTGAGCTCAGCCCTCTCGGAGAAAGAGT 321
 |||||
 QY 244 CCATTCCTCTGGGGCTCTTAAGGGAGTTTGTCTCTACCTGACAAAGATAAGGA 303
 |||||
 Db 322 CCATTCCTCTGGGGCTCTTAAGGGAGTTTGTCTCTACCTGACAAAGATAAGGA 381
 |||||
 QY 304 CAAAGTCATCATCCCTTCAGCTGAGAGAGAGAACTGATGAGCTGGCCCAAG 363
 |||||
 Db 382 CAAAGTCATCATCCCTTCAGCTGAGAGAGAGAACTGATGAGCTGGCCCAAG 441
 |||||
 QY 364 GAATCAGACGCGCGCCCTTCATCTTTATAGGGCTCAGTGGCTCTGGAACATGCTG 423
 |||||
 Db 442 GAATCAGACGCGCGCCCTTCATCTTTATAGGGCTCAGTGGCTCTGGAACATGCTG 501
 |||||
 QY 424 GAGTCGGCGCTCAGCCCGGATGCTCATCTGACCTCGCATTTGTAATGACCTGTT 483
 |||||
 Db 502 GAGTCGGCGCTCAGCCCGGATGCTCATCTGACCTCGCATTTGTAATGACCTGTT 561
 |||||
 QY 484 GGGGTGACAGATAAATTTGAGAACAGAGAAACACATTTGATTTTCATTTCAACCATTTGC 543
 |||||
 Db 562 GGGGTGACAGATAAATTTGAGAACAGAGAAACACATTTGATTTTCATTTCAACCATTTGC 621
 |||||
 QY 544 AAAGCTGAATGAGCCCGCAGTGAAGTCAAGCATTTAG 579
 |||||
 Db 622 AAAGCTGAATGAGCCCGCAGTGAAGTCAAGCATTTAG 657
 |||||
 RESULT 7
 AAC66727
 ID AAC66727 standard; cDNA; 802 BP.
 XX AAC66727;
 AC AAC66727;
 XX
 DT 13-FEB-2001 (first entry)
 XX
 DE Human Interleukin-1 homologue IL-1H4 coding sequence.
 XX
 KW Human; Interleukin-1 homologue; IL-1H4; Inflammation; septicemia;
 KW autoimmune disease; inflammatory bowel disease; psoriasis; arthritis;
 KW transplant rejection; graft versus host disease; infection; stroke;
 KW ischemia; acute respiratory disease; allergy; asthma; restenosis;
 KW brain injury; AIDS; bone disease; osteoporosis; cancer;
 KW congestive heart failure; atherosclerosis; Alzheimer's disease; ss.
 XX
 OS Homo sapiens.
 OS
 PN WO200063226-A1.
 XX
 PD 26-OCT-2000.
 XX
 PF 14-APR-2000; 2000WO-US10207.
 XX
 PR 16-APR-1999; 99US-0293625.
 XX
 PA (SMIR) SMITHKLINE BEECHAM CORP.
 XX
 PI Young PR, McDonnell PC;
 XX
 DR MPI: 2000-687155/67.
 XX
 P-PSDB: AAB28266.
 XX
 PT Interleukin-1 homologue useful for treating conditions such as chronic
 PT and acute inflammation, septicemia, autoimmune diseases ischemia, acute
 PT respiratory disease, allergies, and asthma -
 XX
 PS Claim 2; Page 28; 30pp; English.
 XX
 CC The present sequence is the coding sequence for human interleukin-1
 CC homologue (IL-1H4). IL-1H4 is useful for treating conditions such as
 CC chronic and acute inflammation, septicemia, autoimmune diseases (e.g.
 CC inflammatory bowel disease, psoriasis, and arthritis), transplant

CC rejection, graft versus host disease, infection, stroke, ischemia,
 CC acute respiratory disease, allergies, asthma, restenosis, brain injury,
 CC AIDS, bone diseases (e.g. osteoporosis), cancer, congestive heart
 CC failure, atherosclerosis, and Alzheimer's disease, related to either an
 CC excess of, or an under-expression of, IL-1H4 polypeptide activity.
 CC
 XX
 SQ Sequence 802 BP; 243 A; 190 C; 185 G; 184 T; 0 other.
 Query Match 88.6%; Score 512.8; DB 21; Length 802;
 Best Local Similarity 99.6%; Pred. No. 4.8e-161;
 Matches 514; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 64 AGAGTCCAAAGTGACAGACTTAACCCGAGAAATTCAGCATTCATGACAGATCAC 123
 |||||
 Db 199 ACAAGTCCAAAGTGACAGACTTAACCCGAGAAATTCAGCATTCATGACAGATCAC 258
 |||||
 QY 124 AAAGTACTGCTCTGAGATCTGAGAAATCTCATATGACATTCAGATTAACACTACATAC 183
 |||||
 Db 259 AAAGTACTGCTCTGAGATCTGAGAAATCTCATATGACATTCAGATTAACACTACATAC 318
 |||||
 QY 184 CCAGAGATCTTCTTGGCATTAGCCTCATCTGAGCTCAGCCCTCTCGGAGAAAGAGT 243
 |||||
 Db 319 CCAGAGATCTTCTTGGCATTAGCCTCATCTGAGCTCAGCCCTCTCGGAGAAAGAGT 378
 |||||
 QY 244 CCGATTCCTCTGGGGCTCTTAAGGGAGTTTGTCTCTACTGTAACAAGATAAGGA 303
 |||||
 Db 379 CCGATTCCTCTGGGGCTCTTAAGGGAGTTTGTCTCTACTGTAACAAGATAAGGA 438
 |||||
 QY 304 CAAAGTCATCATCCCTTCAGCTGAGAGAGAACTGATGAGCTGGCCCAAG 363
 |||||
 Db 439 CAAAGTCATCATCCCTTCAGCTGAGAGAGAACTGATGAGCTGGCCCAAG 498
 |||||
 QY 364 GAATCAGACGCGCGCCCTTCATCTTTATAGGGCTCAGTGGCTCTGGAACATGCTG 423
 |||||
 Db 499 GAATCAGACGCGCGCCCTTCATCTTTATAGGGCTCAGTGGCTCTGGAACATGCTG 558
 |||||
 QY 424 GAGTCGGCGCTCAGCCCGGATGCTCATCTGACCTCGCATTTGTAATGACCTGTT 483
 |||||
 Db 559 GAGTCGGCGCTCAGCCCGGATGCTCATCTGACCTCGCATTTGTAATGACCTGTT 618
 |||||
 QY 484 GGGGTGACAGATAAATTTGAGAACAGAGAAACACATTTGATTTTCATTTCAACCATTTGC 543
 |||||
 Db 619 GGGGTGACAGATAAATTTGAGAACAGAGAAACACATTTGATTTTCATTTCAACCATTTGC 678
 |||||
 QY 544 AAAGCTGAATGAGCCCGCAGTGAAGTCAAGCATTTAG 579
 |||||
 Db 679 AAAGCTGAATGAGCCCGCAGTGAAGTCAAGCATTTAG 714
 |||||
 RESULT 8
 AAF84120
 ID AAF84120 standard; cDNA; 802 BP.
 XX AAF84120;
 AC AAF84120;
 XX
 DT 22-AUG-2001 (first entry)
 XX
 DE Interleukin-1 homologue (IL-1H4) polypeptide encoding cDNA.
 XX
 KW Interleukin-1; IL-1H4; antiinflammatory; antibacterial; antiallergic;
 KW immunosuppressive; antipsoriatic; antiarthritic; cycostatic; antiHIV;
 KW cerebroprotective; antidiabetic; vasotropic; vulnerary; osteopachic;
 KW immunostimulant; antiarteriosclerotic; nootropic; neuroprotective;
 KW gene therapy; vaccine; ss.
 XX
 OS Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FH CDS 58..714
 FT /*tag= a
 FT /product= "IL-1H4"
 FT sig_peptide 58..117
 FT /*tag= b

FT mat_peptide 118..711
 FT /*tag= c
 XX
 XX MO200140247-A1.
 XX
 XX 07-JUN-2001.
 XX
 XX 30-NOV-2000; 2000WO-US32521.
 XX
 XX 01-DEC-1999; 99US-0452140.
 XX
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 XX Kumar S, McDonnell PC, Young PR;
 XX
 XX WPI: 2001-389949/41.
 XX
 XX P-PSDB: AAB85136.
 XX
 XX Novel interleukin-1 homolog, IL-1H4, for treating chronic and acute
 PT inflammation, septicemia, autoimmune diseases, transplant rejection,
 PT graft versus host disease, stroke, ischemia, allergy and asthma
 XX
 XX Examples; Page 29; 30pp; English.
 XX
 XX The invention provides an isolated interleukin-1 homologue, IL-1H4
 CC polypeptide. The IL-1H4 polypeptide can be expressed by standard
 CC recombinant methodology. The IL-1H4 polypeptide, polynucleotides and
 CC modulators are useful for treating chronic and acute inflammation,
 CC septicemia, autoimmune diseases (e.g., inflammatory bowel disease,
 CC psoriasis and arthritis), transplant rejection, graft versus host
 CC disease, infection, stroke, ischemia, acute respiratory disease syndrome,
 CC allergies, asthma, restenosis, brain injury, AIDS, bone diseases (e.g.,
 CC osteoporosis), cancer (e.g., lymphoproliferative disorders), congestive
 CC heart failure, atherosclerosis and Alzheimer's disease. The IL-1H4
 CC polynucleotides are useful as diagnostic reagents and for chromosome
 CC identification. The present sequence represents the cDNA encoding the
 CC IL-1H4 polypeptide of the invention.
 XX
 XX Sequence 802 BP; 243 A; 190 C; 185 G; 184 T; 0 other;

Query Match 88.6%; Score 512.8; DB 22; Length 802;
 Best Local Similarity 99.6%; Pred. No. 4.8e-161;

Matches 514; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 AGAGTCCAAAGTGAGACTTAACCCGAGAAATTCAGATCTGTGACCGAGATCAC 123
 DB 199 ACAAGTCCAAAGTGAGAACTTAACCCGAGAAATTCAGATCTGTGACCGAGATCAC 258
 QY 124 AAATGACTGCTCGAGACTCGGAGATCTCATAGACATTCAGATAAACTCATACGCG 183
 DB 259 AAATGACTGCTCGAGACTCGGAGATCTCATAGACATTCAGATAAACTCATACGCG 318
 QY 184 CCAGAGATCTTTCATTAAGCTCATCCCTGAGCTCAGCTCGGAGAAAGAGT 243
 DB 319 CCAAGAGATCTTTCATTAAGCTCATCCCTGAGCTCAGCTCGGAGAAAGAGT 378
 QY 244 CCGATTCCTCGGGGGGCTCTAAAGGGAGTTTGTCTACTGTGACCAAGATAAGGA 303
 DB 379 CCGATTCCTCGGGGGGCTCTAAAGGGAGTTTGTCTACTGTGACCAAGATAAGGA 428
 QY 304 CAAAGTATCCATCCCTTCAGCTGAAGAGAGAGAACTGATGAAGCTGCGCCAAAG 363
 DB 439 CAAAGTATCCATCCCTTCAGCTGAAGAGAGAGAACTGATGAAGCTGCGCCAAAG 498
 QY 364 GAATCAGACAGCGCGCCCTTCATTTTATAGGCTCAGTGGGCTCTCGAATATGCTG 423
 DB 499 GAATCAGACAGCGCGCCCTTCATTTTATAGGCTCAGTGGGCTCTCGAATATGCTG 558
 QY 424 GAGTCGGGGGCTCACCCCGATGGTTCATGACACCTCGCATATGTAAGCCGTT 483
 DB 559 GAGTCGGGGGCTCACCCCGATGGTTCATGACACCTCGCATATGTAAGCCGTT 618
 QY 484 GGGGTGACAGATTAATTTGAGAACAGAAACATTAATTTTCAACAGTTTGC 543

DB 619 GGGGTGACAGATTAATTTGAGAACAGAAACATTAATTTTCAACAGTTTGC 678
 QY 544 AAAGCTGAATAGAGCCCGAGTGAAGTCAAGCAATTGAG 579
 DB 679 AAAGCTGAATAGAGCCCGAGTGAAGTCAAGCAATTGAG 714

RESULT 9

AAAS1604
 ID AAAS1604 standard; DNA; 839 BP.

AAAS1604;

31-OCT-2000 (first entry)

Human IL-1 receptor antagonist 1 V DNA.

hIL-1Ra1v; human interleukin-1 receptor antagonist-1; IL-11p;
 KW osteopathic; interleukin-1-like polypeptide; anti-inflammatory;
 KW anti-asthmatic; anti-arthritis; antimicrobial; respiratory; vaccine;
 KW anti-ischemic; dermatological; immunomodulatory; gastrointestinal;
 KW gene therapy; ds.

Homo sapiens.

Key Location/Qualifiers

CDS 73..729

/*tag= a
 /product= hIL-1Ra1v
 /partial

MO200039297-A2

06-JUL-2000.

22-DEC-1999; 99WO-US30720.

23-DEC-1998; 98US-0113430.

22-JAN-1999; 99US-011843.

13-APR-1999; 99US-0129122.

(GENENTECH INC.

Goddard A, Pan J;
 WPI: 2000-452395/39.

P-PSDB; AAY96940.

Nucleic acids encoding interleukin-1-like polypeptides, useful for
 preventing and treating e.g. inflammation, asthma and psoriasis

Claim 7; Fig 19; 143pp; English.

An isolated nucleic acid molecule encoding an interleukin-1-like
 polypeptide (IL-11p) that retains one or more activities of the peptide
 from which it is derived, such as the IL-18R binding activity of a human
 interleukin-1 receptor antagonist-1 (hIL-1Ra1) polypeptide, is new. The
 nucleic acids may be used in molecular engineering applications, e.g.
 hybridization assays and chromosome and gene mapping studies, for
 recombinantly producing the IL-11p polypeptide or for producing gene
 knock out animals to study the role of the protein in metabolism and
 disease processes (conversely, gene therapy protocols may be used to
 supplement a patient's production of the polypeptide or to rectify
 mutations that lead to the production of in active peptides). The
 peptides produced may be used to screen for and produce modulators (e.g.
 antibodies) of IL-11p protein expression and activity which may be use
 to treat disorders associated with inappropriate IL-11p expression and
 activity, such as inflammatory disorders, asthma, arthritis,
 osteoarthritis, sepsis, acute lung injury, adult respiratory distress
 syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
 psoriasis, graft versus host disease and/or inflammatory bowel disease.

KW Human; interleukin 1; IL-1; growth factor; Tango-77; diagnosis;
 KW Identification; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 370..1026
 FT CDS /*tag= a
 FT /product= "IL-1 family protein"
 XX
 PN JP2001231578-A.
 XX
 PD 28-AUG-2001.
 XX
 PE 07-DEC-2000; 2000JP-0372864.
 XX
 PR 09-DEC-1999; 99JP-0349780.
 XX
 PA (XYOW) KYOWA HAKKO KOGYO KK.
 XX
 DR WPI: 2001-609968/70.
 DR P-PSDB: AAG68116.
 XX
 PT An IL-1 family protein, used for the development of diagnostic and
 PT treatment agents -
 XX
 PS Claim 2; Page 31-32; 38pp; Japanese.
 XX
 CC The present sequence encodes a human interleukin 1 (IL-1) family
 CC protein having a combining affinity to a receptor of a protein of
 CC human IL-1 family higher than Tango-77. The protein is useful for the
 CC development of diagnostic, treating and/or preventive agents for
 CC various diseases.
 XX
 SQ Sequence 1104 BP; 328 A; 258 C; 255 G; 263 T; 0 other;
 Query Match 88.6%; Score 512.8; DB 22; Length 1104;
 Best Local Similarity 99.6%; Pred. No. 5,7e-161;
 Matches 514; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 64 AGAGTCCAAAGGTGAGAACTTAAACCCGAGAAATTCAGATTCATGACCGATCAC 123
 DB 511 ACAAGTCCAAAGGTGAGAACTTAAACCCGAGAAATTCAGATTCATGACCGATCAC 570
 OY 124 AAAGTACTGCTGCTGAGATCTGGAAATCTATAGCAGTCCAGATAAACTACATACGC 183
 DB 571 AAAGTACTGCTGCTGAGATCTGGAAATCTATAGCAGTCCAGATAAACTACATACGC 630
 OY 184 CCAGAGATCTTCTTGCAATTAGCCTCATCTTGAGCTCAGCCTCTGGGAGAAAGAGT 243
 DB 631 CCAGAGATCTTCTTGCAATTAGCCTCATCTTGAGCTCAGCCTCTGGGAGAAAGAGT 690
 OY 244 CCGATTCCTCGGGGGTCTTAAAGGAGATTGTCTCTACTCTGACAAAGATTAAGA 303
 DB 691 CCGATTCCTCGGGGGTCTTAAAGGAGATTGTCTCTACTCTGACAAAGATTAAGA 750
 OY 304 CAAATCATCCATCCCTTACAGCTGAAGAGAGAACTGATGAGAGCTGGCTGCCAAAG 363
 DB 751 CAAATCATCCATCCCTTACAGCTGAAGAGAGAACTGATGAGAGCTGGCTGCCAAAG 810
 OY 364 GAATCAGACGCCGGCCCTTATCTTTATAGGCTCAGTGGGCTCCTTGAAACATGCTG 423
 DB 811 GAATCAGACGCCGGCCCTTATCTTTATAGGCTCAGTGGGCTCCTTGAAACATGCTG 870
 OY 424 GAGTGGGGGCTCAACCCCGATGATCTGCACTCCCTGCAATTTGTAATGAGACCTGTT 483
 DB 871 GAGTGGGGGCTCAACCCCGATGATCTGCACTCCCTGCAATTTGTAATGAGACCTGTT 930
 OY 484 GGGGTGACAGATTAATTTGAGAACAGAGAAACATTTGATTTCAACAGATTGC 543
 DB 931 GGGGTGACAGATTAATTTGAGAACAGAGAAACATTTGATTTCAACAGATTGC 990
 OY 544 AAAGTGAATGAGCCCAAGTGAAGTCAAGCATTAAG 579

DB 991 AAAGTGAATGAGCCCAAGTGAAGTCAAGCATTAAG 1026
 RESULT 12
 AAD00210
 ID AAD00210 standard; cDNA; 1600 BP.
 XX
 AC AAD00210;
 XX
 DT 05-SEP-2000 (first entry)
 XX
 DE Human zilla4 cDNA.
 XX
 KW Human interleukin-1; IL-1; zilla4 protein; inflammation; arthritis;
 KW psoriasis; septic shock; graft-versus-host disease; leukemia; cancer;
 KW anaemia; inflammatory bowel disease; acute neuropathology; shock;
 KW chronic neuropathology; respiratory disease syndrome; restenosis;
 KW acquired immune deficiency syndrome; AIDS; anti-inflammatory; cytostatic;
 KW anti-arthritis; anti-psoriasis; antibacterial; immunosuppressive;
 KW anti-anaemic; neuroprotective; vasotrophic;
 KW anti-human immunodeficiency virus; HIV; SS.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 847..1503
 FT CDS /*tag= a
 FT /product= "Human zilla4 protein"
 XX
 PN WQ200024899-A2.
 XX
 PD 04-MAY-2000.
 XX
 PE 27-OCT-1999; 99WO-US25038.
 XX
 PR 27-OCT-1998; 98US-0179614.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI West RR, Sheppard PO, Gao Z;
 DR WPI: 2000-350740/30.
 DR P-PSDB: AAY70927.
 XX
 PT Immunomodulatory interleukin-1 homolog zilla4 proteins, useful for
 PT treatment of e.g. arthritis, psoriasis, septic shock, graft-versus-host
 PT disease, leukemia -
 XX
 PS Example 2; Page 61-63; 88pp; English.
 XX
 CC The present cDNA sequence encodes human interleukin (IL)-1 homolog zilla4
 CC protein. This cDNA was cloned from a human foetal lung cDNA library. The
 CC zilla4 proteins modulate inflammation and other immunological
 CC processes and are therefore useful for treatment of arthritis, psoriasis,
 CC septic shock, graft-versus-host disease and leukaemia. Other diseases
 CC that may be modulated by zilla4 proteins include cancer, anaemia,
 CC inflammatory bowel disease, acute and chronic neuropathologies, shock,
 CC respiratory disease syndrome, restenosis and acquired immune deficiency
 CC syndrome.
 XX
 SQ Sequence 1600 BP; 481 A; 356 C; 378 G; 385 T; 0 other;
 Query Match 88.6%; Score 512.8; DB 21; Length 1600;
 Best Local Similarity 99.6%; Pred. No. 7e-161;
 Matches 514; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 64 AGAGTCCAAAGGTGAGAACTTAAACCCGAGAAATTCAGATTCATGACCGATCAC 123
 DB 988 ACAAGTCCAAAGGTGAGAACTTAAACCCGAGAAATTCAGATTCATGACCGATCAC 1047
 OY 124 AAAGTACTGCTGCTGAGATCTGGAAATCTATAGCAGTTCAGATTAACATCACTACGC 183

```
Db 1048 AAAGTACGTCGCTGAGACTGCGAATCATAGACACTTCCAGATAAAACTACATAGCC 1107
QY 184 CCAGAGATCTTCTTTCATTAAGCCTCATCCTTGAGCTACAGCCTCTGCGGAGAAAGAGT 243
Db 1108 CCAGAGATCTTCTTTCATTAAGCCTCATCCTTGAGCTACAGCCTCTGCGGAGAAAGAGT 1167
QY 244 CCGATTCCTCCGGGGGCTCTAAAGGGAGTTTGTCTACGTGTGACAAAGATTAAGGA 303
Db 1168 CCGATTCCTCCGGGGGCTCTAAAGGGAGTTTGTCTACGTGTGACAAAGATTAAGGA 1227
QY 304 CAAAGTCATCCATCCCTTCAGCTGAGAGAGAAAGAACTGAAAGCTGAGCTGCCCAAAAG 363
Db 1228 CAAAGTCATCCATCCCTTCAGCTGAGAGAGAAAGAACTGAAAGCTGAGCTGCCCAAAAG 1287
QY 364 GAATCAGACAGCGCGGCTTCATCTTTTATAGGCTCAGGTGGCTCTGGAACATGCTG 423
Db 1288 GAATCAGACAGCGCGGCTTCATCTTTTATAGGCTCAGGTGGCTCTGGAACATGCTG 1347
QY 424 GAGTCGGCGGCTACCCCGGATGTTTCATCTGACCTCCTGCAATTGTATGAGCTGTT 483
Db 1348 GAGTCGGCGGCTACCCCGGATGTTTCATCTGACCTCCTGCAATTGTATGAGCTGTT 1407
QY 484 GGGGTGACAGATAAATTGAGAACAGAGAAACACATTTGAAATTTTCATTTCAACCATTTGC 543
Db 1408 GGGGTGACAGATAAATTGAGAACAGAGAAACACATTTGAAATTTTCATTTCAACCATTTGC 1467
QY 544 AAAGCTGAATGAGCCCGCACTGAGTACGATTTAG 579
Db 1468 AAAGCTGAATGAGCCCGCACTGAGTACGATTTAG 1503

RESULT 13
ID AAAS1601 standard; DNA; 626 BP.
XX
AC AAAS1601;
XX
DT 31-OCT-2000 (first entry)
XX
DE Human IL-1 receptor antagonist 1 long DNA.
XX
KW hIL-1Ralpha; human interleukin-1 receptor antagonist-1 long; IL-11p;
KW osteopathic; interleukin-1-like polypeptide; anti-inflammatory;
KW anti-asthmatic; anti-arthritis; antimicrobial; respiratory; vaccine;
KW anti-ischemic; dermatological; immunomodulatory; gastrointestinal;
KW gene therapy; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 4.626
FT FT /*tag= a
FT FT /product= hIL-1Ralpha
FT FT /partial
XX
PN WO200039297-A2.
XX
PD 06-JUL-2000.
XX
PF 22-DEC-1999; 99WO-US30720.
XX
PR 23-DEC-1998; 98US-0113430.
PR 22-JAN-1999; 98US-0116843.
PR 13-APR-1999; 99US-0129122.
XX
PA (GETH ) GENENTECH INC.
XX
PI Goddard A, Pan J;
XX
DR WPI: 2000-452395/39.
DR P-PSDB: AAY96938.
XX
PT Nucleic acids encoding interleukin-1-like polypeptides, useful for
```

```
PT preventing and treating e.g. inflammation, asthma and psoriasis
XX
XX Claim 7; Fig 15; 143pp; English.
XX
CC An isolated nucleic acid molecule encoding an interleukin-1-like
CC polypeptide (IL-11p) that retains one or more activities of the peptide
CC from which it is derived, such as the IL-18R binding activity of a human
CC interleukin-1 receptor antagonist-1 (hIL-1Ralpha) polypeptide, is new. The
CC nucleic acids may be used in molecular engineering applications, e.g.
CC hybridization assays and chromosome and gene mapping studies, for
CC recombinantly producing the IL-11p polypeptide or for producing gene
CC knock out animals to study the role of the protein in metabolism and
CC disease processes (conversely, gene therapy protocols may be used to
CC supplement a patient's production of the polypeptide or to rectify
CC mutations that lead to the production of in active peptides). The
CC peptides produced may be used to screen for and produce modulators (e.g.
CC antibodies) of IL-11p protein expression and actively which may be use
CC to treat disorders associated with inappropriate IL-11p expression and
CC activity, such as inflammatory disorders, asthma, arthritis,
CC osteoarthritis, sepsis, acute lung injury, adult respiratory distress
CC syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
CC psoriasis, graft versus host disease and/or inflammatory bowel disease.
XX
SQ Sequence 626 BP; 178 A; 154 C; 153 G; 141 T; 0 other;

Query Match 88.4%; Score 511.8; DB 21; Length 626;
Best Local Similarity 99.6%; Pred. No. 9e-161.
Matches 513; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 AGAGTCCAAAGGTGAAGACTTAACCCGAGAAATTCAGCATTCATGACAGATCAC 123
Db 112 ACAAGTCCAAAGGTGAAGACTTAACCCGAGAAATTCAGCATTCATGACAGATCAC 171
QY 124 AAAGTACGTGCTCGGAGTCTGGAGATCTCTATGACAGTTCAGATTAAGAACTACATGCC 183
Db 172 AAAGTACGTGCTCGGAGTCTGGAGATCTCTATGACAGTTCAGATTAAGAACTACATGCC 231
QY 184 CCAGAGATCTTCTTTCATTAAGCTTACCTCATCTTTCAGCTCAGCTGCGGAGAAAGAGT 243
Db 232 CCAGAGATCTTCTTTCATTAAGCTTACCTCATCTTTCAGCTCAGCTGCGGAGAAAGAGT 291
QY 244 CCGATTCCTCCGGGGGCTCTAAAGGGAGTTTGTCTACGTGTGACAAAGATTAAGGA 303
Db 292 CCGATTCCTCCGGGGGCTCTAAAGGGAGTTTGTCTACGTGTGACAAAGATTAAGGA 351
QY 304 CAAAGTCATCCATCCCTTCAGCTGAGAGAGAAAGAACTGAAAGCTGAGCTGCCCAAAAG 363
Db 352 CAAAGTCATCCATCCCTTCAGCTGAGAGAGAAAGAACTGAAAGCTGAGCTGCCCAAAAG 411
QY 364 GAATCAGACAGCGCGGCTTCATCTTTTATAGGCTCAGGTGGCTCTGGAACATGCTG 423
Db 412 GAATCAGACAGCGCGGCTTCATCTTTTATAGGCTCAGGTGGCTCTGGAACATGCTG 471
QY 424 GAGTCGGCGGCTACCCCGGATGTTTCATCTGACCTCCTGCAATTGTATGAGCTGTT 483
Db 472 GAGTCGGCGGCTACCCCGGATGTTTCATCTGACCTCCTGCAATTGTATGAGCTGTT 531
QY 484 GGGGTGACAGATAAATTGAGAACAGAGAAACACATTTGAAATTTTCATTTCAACCATTTGC 543
Db 532 GGGGTGACAGATAAATTGAGAACAGAGAAACACATTTGAAATTTTCATTTCAACCATTTGC 591
QY 544 AAAGCTGAATGAGCCCGCACTGAGTACGATTTAG 578
Db 592 AAAGCTGAATGAGCCCGCACTGAGTACGATTTAG 626

RESULT 14
AADD00212
ID AADD00212 standard; cDNA; 657 BP.
XX
AC AADD00212;
XX
DT 05-SEP-2000 (first entry)
```

DE	XX
Human zllla4-E200K variant cDNA.	
KW	Human interleukin-1; IL-1; zlll4 protein; inflammation; arthritis;
KM	psoriasis; septic shock; graft-versus-host disease; leukaemia; cancer;
KV	anemia; inflammatory bowel disease; acute neuropathology; shock;
KW	chronic neuropathology; respiratory disease syndrome; restenosis;
KW	acquired immune deficiency syndrome; AIDS; antineoplastic cytosolic
KW	anti-arthritis; anti-psoriatic; antibacterial; immunosuppressive;
KW	anti-neutrophic; neuroprotective; vasotropic;
KW	anti-human immunodeficiency virus; HIV; ss-
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	CDS 1..657
FT	/tag= a
FT	/product= "zlll4-E200K protein"
FT	.
FT	unsure 598..600
FT	/tag= b
FT	/product= "Encodes Lys"
XX	
PN	WO200024899-A2.
PD	04-MAY-2000.
PE	27-OCT-1999; 99WO-US25038.
PR	27-OCT-1998; 98US-0179614.
PA	(ZYMO) ZYMOGENETICS INC.
PI	West RR, Shepard PO, Gao Z;
DR	WPJ: 2000-350740/30.
PS	P-PSDB; AAY70933.
PT	Immunomodulatory Interleukin-1 homolog zlll4 proteins, useful for
PT	treatment of e.g. arthritis, psoriasis, septic shock, graft-versus-host
PT	disease, leukemia -
XX	
PS	Disclosure; Page 76-77; 88pp; English.
CC	The present cDNA sequence encodes a variant of human interleukin (IL)-1
CC	homolog zlll4 protein designated zlll4-E200K. The replacement of
CC	Glu (200) with Lys results in change in activity from agonist to
CC	antagonist. The zlll4 proteins modulate inflammation and other
CC	immunological processes and are therefore useful for treatment of
CC	arthritis, psoriasis, septic shock, graft-versus-host disease and
CC	leukemia. Other diseases that may be modulated by zlll4 proteins
CC	include cancer, anemia, inflammatory bowel disease, acute and chronic
CC	neuropathologies, shock, respiratory disease syndrome, restenosis and
CC	acquired immune deficiency syndrome.
XX	
XO	Sequence 657 BP; 185 A; 158 C; 165 G; 148 T; 1 other:
Query Match	88.2%; Score 510.8; DB 21; Length 657;
Best Local Similarity	99.2%; Pred. No. 2e-160;
Matches 512; Conservative % 1; Mismatches 3; Indels 0; Gaps	
OY	64 AGAGSTCCAAGGGGGAAGAATTAAACCGCAGAAATTCAGCATTCATGCAGAGTACC 123 Db 142 ACAAGTCCAAAAGGTGAAGAACCTTAACCCGCAAGAAATAATTCAGCATTCATGCAGAGTACC 201 124 AAATACTAGTGCCGTGGAGCTGGGAATCTCATPACAGTTCCAGTAAANACTAATACGCC 183 Db 202 AAAAGTAGTGCTGAGACTGGGAATCTCATPACAGTTCCAGTAAANACTAATACGCC 261 184 CCAGAGATCTCTTGGATTAAGCTCACNCCTTGAGCTCAGCCTCGGGGAGAAAGGAGT 243 Db 262 CCAGAGATCTCTTGGATTAAGCTCACNCCTTGAGCTCAGCCTCGGGGAGAAAGGAGT 321 244 CGGATTCCTCGGGGAGTCTTAAAGGGGAGTGTGTTCTCTACTGTCGACAAGATTAAGGA 303

Db	322	CGATTTCCTCGGGGCTCTAAAGGGAGTTTGTCTACTGTGACAAAGATAAAGA	381
QY	304	CAAAATCATCATCCTTACGCTGAAGAGAGAAACTGATGAAGCTGGCTGCCCAAAAG	363
Db	382	CAAAATCATCATCCTTACGCTGAAGAGAGAAACTGATGAAGCTGGCTGCCCAAAAG	441
QY	364	GAATCAGCAGCCCGCCCTTCATCTTTTAAAGGGCTCAGGTGGGCTCTGGAACATGCTG	423
Db	442	GAATCAGCAGCCCGCCCTTCATCTTTTAAAGGGCTCAGGTGGGCTCTGGAACATGCTG	501
QY	424	GAGTGGGCGCTCAACCCGGATGTTATGCACTCTCGCAATTTGATAGCCTGTT	483
Db	502	GAGTGGGCGCTCAACCCGGATGTTATGCACTCTCGCAATTTGATAGCCTGTT	561
QY	484	GGGGTGACAGATTAATTTGAGAACAGGAACACATGTAATTTTCATTCAACAGCTTGC	543
Db	562	GGGGTGACAGATTAATTTGAGAACAGGAACACATGTAATTTTCATTCAACAGCTTGC	621
QY	544	AAAGCTGAATGAGCCCCAGTGAAGTCAAGCATTTAG	579
Db	622	AAAGCTGAATGAGCCCCAGTGAAGTCAAGCATTTAG	657
RESULT 15			
ID	AAAC84317	AAC84317 standard; cDNA; 630 BP.	
XX	AC	AAC84317;	
XX	DT	19-MAR-2001 (first entry)	
XX	DE	Human EXCS encoding cDNA (clone ID 4365383CB1).	
KW	EXtracellular signaling molecule; EXCS; anti-inflammatory; human;		
KW	Immunosuppressive; cytostatic; neuroprotective; gastrointestinal;		
KW	virucide; antibacterial; anti-HIV; human immunodeficiency virus;		
KW	antifertility; cerebroprotective; nootropic; antifungal; antifungal;		
KW	anticonvulsant; tranquilizer; neuroleptic; vasotropic; gynecological;		
KW	keratolytic; protozoacide; gene therapy; ss.		
OS	Homo sapiens.		
XX	XX	WO200070049-A2.	
XX	PD	23-NOV-2000.	
XX	PF	19-MAY-2000; 2000WO-US13975.	
XX	PR	19-MAY-1999; 99US-0134949.	
XX	PR	15-JUL-1999; 99US-0144270.	
XX	PR	30-JUL-1999; 99US-0146700.	
XX	PR	04-OCT-1999; 99US-0157508.	
XX	PA	(INCY-) INCYTE GENOMICS INC.	
XX	PI	Tang YT, Yoe H, Lal P, Burford N, Bandman O, Baughn MR;	
XX	PI	Azimzai Y, Lu DAM, Patterson C;	
XX	DR	WPI: 2001-025021/03.	
XX	DR	P-PSDB: AAB48081.	
PT	PT	New human extracellular signaling nucleic acids and polypeptides useful	
PT	PT	for diagnosing, treating and preventing infections and	
PT	PT	gastrointestinal, neurological, reproductive, and	
XX	XX	autoimmune/inflammatory disorders -	
PS	PS	Claim 4; Page 112; 114pp; English.	
CC	CC	The invention provides human extracellular signaling molecules (EXCS)	
CC	CC	and polynucleotides which identify and encode EXCS. EXCS can be	
CC	CC	expressed by standard recombinant methodology. The amino acid and nucleic	
CC	CC	acid sequences of EXCS are useful for diagnosing, treating and	

CC preventing infections and gastrointestinal (peptic ulcer, dysphagia, pancreatitis), neurological (e.g. epilepsy, ischemic cerebrovascular disease, stroke), reproductive (infertility, ovulatory defects, endometriosis), autoimmune/inflammatory (actinic keratosis, acquired immunodeficiency syndrome (AIDS), Addison's disease), and cell proliferative disorders including cancers (of the breast, adrenal gland, bone). They may also be used to treat fatal familial insomnia, nutritional and metabolic diseases of the nervous system, myopathies, mental disorders (anxiety, schizophrenia, mood), as well as infections caused by parasites (malaria, leishmania, trypanosoma), viral (adenovirus, coronavirus, flavivirus), bacterial (e.g. pneumococcus, staphylococcus, bacillus), and fungal (aspergillus, blastomycosis, dermatophytes) agents. The nucleic acids, polypeptides, antagonists, agonists, pharmaceutical compositions, and antibodies may also be used for treating or preventing disorders associated with increased or decreased expression or activity of EXCS. EXCS polynucleotides may also be used to detect and quantify gene expression in biopsied tissues in which expression of EXCS may be correlated with the disease, to determine presence or excess expression of EXCS, to monitor regulation of EXCS levels during therapeutic intervention, to detect the presence of associated disorders, as targets in microarray, to generate hybridization probes, and to detect differences in gene sequences among normal, carrier or affected individuals. Antibodies may also be used in diagnosing disorders, in monitoring patients being treated with EXCS agonists, antagonists or inhibitors. Sequences AAC84293-C84318 represent nucleic acid molecules encoding the EXCS of the invention.

xx
SQ Sequence 630 BP; 185 A; 156 C; 141 G; 148 T; 0 other;

Query Match 88.0%; Score 509.6; DB 22; Length 630;
Best Local Similarity 99.2%; Pred. No. 4.9e-160;

Matches 512; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 64 AGAGGCCAAAGTGAAGACTTAACCGGAGAAATTCAGATTCATGACCAGATCAC 123
DB 37 ACAGGTCGAAAGGTGAAGCGTTAAACCGAAGAAATTCAGATTCATGACCAGATCAC 96
QY 124 AAAGTACTGCTCTGACTCTGGGATCTCATAGCAGTTCAGATAAAACTATACGC 183
DB 97 AAAGTACTGCTCTGACTCTGGGATCTCATAGCAGTTCAGATAAAACTATACGC 156
QY 184 CCAGAGATTTCTTGTGATTAAGCTCATCTTGAAGCTCAGCTCGGAGAGAAAGT 243
DB 157 CCAGAGATTTCTTGTGATTAAGCTCATCTTGAAGCTCAGCTCGGAGAGAAAGT 216
QY 244 CCGATTCTCTGGGGGCTCTTAAGGGAGTTTGTCTCTACTGTGACAAGATTAAGA 303
DB 217 CCGATTCTCTGGGGGCTCTTAAGGGAGTTTGTCTCTACTGTGACAAGATTAAGA 276
QY 304 CAAAGTCATCATCTCTTCAAGTGAAGAGAACTGATGAACTGGTGCCTCCAAAG 363
DB 277 CAAAGTCATCATCTCTTCAAGTGAAGAGAACTGATGAACTGGTGCCTCCAAAG 336
QY 364 GAATCAGCACGGCGGCTCTCATCTTTATAGGCTCAGGTGGCTCCTGGACATGCTG 423
DB 337 GAATCAGCACGGCGGCTCTCATCTTTATAGGCTCAGGTGGCTCCTGGACATGCTG 396
QY 424 GAGTGGGCGGCTCACCGGATGTTCACTCCTGCAATTTGTAATGAGCGTGT 483
DB 397 GAGTGGGCGGCTCACCGGATGTTCACTCCTGCAATTTGTAATGAGCGTGT 456
QY 484 GGGGTGACAGATAATTGAGAACAGAAACATTTGATTTTCAATTTCAACCACTTGC 543
DB 457 GGGGTGACAGATAATTGAGAACAGAAACATTTGATTTTCAATTTCAACCACTTGC 516
QY 544 AAAGCTGAATGAGCCCAAGTGAAGTCAAGCTGAGTCAAGCTGAGTCAAGCTGAG 579
DB 517 AAAGCTGAATGAGCCCAAGTGAAGTGAAGTCAAGCTGAGTCAAGCTGAGTCAAG 552

Search completed: May 3, 2003, 05:32:32
Job time : 233 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 3, 2003, 05:20:27 ; Search time 1503 Seconds
(without alignments)
6238.980 Million cell updates/sec

Title: US-09-876-790-1

Perfect score: 579
Sequence: 1 atgcacagctcgtatagagag.....ccagtgcagtcagcagattag 579

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

EST:*
1: em_estdb:*
2: em_esthm:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rdg:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	492	85.0	561	9	AI343258
2	429.4	74.2	767	12	BG620449
3	407	70.3	485	9	AI014548
4	223.4	38.6	316	17	AQ041691
5	51.2	8.8	1219	11	AK009787
6	48.6	8.4	870	12	BF244205

7	40.6	7.0	1051	11	AK009741	Mus muscu
8	40.6	7.0	1199	11	AK008977	Mus muscu
9	40.6	7.0	1531	11	AK010020	Mus muscu
10	40.6	7.0	2843	11	AK014576	Mus muscu
11	38.4	6.6	369	9	AI094892	gal13f01.x
12	38.2	6.6	288	14	BQ479845	Iaa70908.
13	37.8	6.5	436	10	AW361164	RC1-CT025
14	37.8	6.5	539	10	AW368430	CM3-HT019
15	37.8	6.5	555	10	AW361172	RC1-CT025
16	37.8	6.5	555	12	BE695960	RC1-CT025
17	37.8	6.5	557	10	AW368437	CM3-HT019
18	37.4	6.5	524	14	BQ968703	QHB34013.
19	37.4	6.5	230	17	AZ094009	RPCL-23-4
20	37.4	6.4	833	17	BH156690	EMTSR85TF
21	36.8	6.4	373	9	AI401773	th23h05.x
22	36.8	6.4	379	10	AW043814	wy81b09.x
23	36.8	6.4	454	9	AI275767	qv67d07.x
24	36.6	6.3	469	14	BQ768134	EBR008-SQ
25	36.6	6.3	1020	12	BG245180	602357579
26	36.4	6.3	375	9	AI220203	q984907.x
27	36.2	6.3	348	9	AI141656	ot08a05.x
28	36.2	6.3	406	17	AZ621717	1M0455A18
29	36.2	6.3	530	13	BM367565	NTIV-051-
30	36.2	6.3	559	10	AW578451	RC1-CT025
31	36.2	6.3	658	13	B1490370	603031838
32	36.2	6.3	672	13	B1826186	603076358
33	36.2	6.2	554	12	BG863310	602798918
34	36	6.2	683	17	CNS04FCT	Retradon
35	35.8	6.2	456	9	AI363086	qy54g04.x
36	35.8	6.2	874	9	AU067032	AU067032
37	35.4	6.1	380	17	BH449868	BH449868
38	35.4	6.1	435	14	W78043	B05JL15TF
39	35.4	6.1	442	9	AI863846	zdf2d01.r1
40	35.4	6.1	578	17	BH714506	w154f08.x
41	35.4	6.1	585	17	BH494058	BOG2538TF
42	35.4	6.1	593	17	BH481439	BOHBL37TR
43	35.4	6.1	646	17	BH668410	BOHES13TF
44	35.4	6.1	680	17	BH589224	BOGVL33TF
45	35.4	6.1	683	17	BH546506	BOGQ377TF

ALIGNMENTS

RESULT 1
AI343258/c 561 bp mRNA linear EST 18-MAR-1999
LOCUS LB94B05.x1 NCI_CGAP_Col6 Homo sapiens cDNA clone IMAGE:2061969 3',
DEFINITION mRNA sequence.
ACCESSION AI343258
VERSION AI343258.1 GI:4080464
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
1 (bases 1 to 561)
TITILE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
AUTHORS Tumor Gene Index
CONTACT: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.
JOURNAL Ph.D.
COMMENT ' cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.lnll.gov/bdrp/image/image.html
Insert Length: 814 Std Error: 0.00
Seq primer: -40UP from Gibco


```

OY 541 TGCAGGCTGAAA 553
DB 625 TGCAGGCTGAAA 637

RESULT 3
AI014548/c 485 bp mRNA linear EST 27-AUG-1998
LOCUS 0n40f01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
DEFINITION IMAGE:1628761.3, mRNA sequence.
ACCESSION AI014548
VERSION AI014548
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 485)
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: c9apds-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (infoimage.lnl.gov) for further information.
Insert Length: 1052 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 424.
FEATURES
source
1. .485
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1628761"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site.1: Not I; Site.2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NDHL19W, testis NHT, and B-cell
NCL-GAP-GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonalogo.
BASE COUNT 117 a 112 c 119 g 137 t
ORIGIN
Query Match 70.3%; Score 407; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.5e-107;
Matches 407; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 173 ACTACATAGGCCCAAGAGATCTTTCATAGCTCCTAGCTCAGCTCTGCG 232
DB 485 ACTACATAGGCCCAAGAGATCTTTCATAGCTCCTAGCTCAGCTCTGCG 426

OY 233 AGAAGAAGTCCGATTTCTCTGGGGGCTCTAAAGGGAGTTTGTCTACTGTGACA 292
DB 425 AGAAGAAGTCCGATTTCTCTGGGGGCTCTAAAGGGAGTTTGTCTACTGTGACA 366

OY 293 AGGATTAAGAGCAAAAGTATCCATCCCTTACAGCTGAAGAGAGAACTGATGAAGCTGG 352
DB 365 AGGATTAAGAGCAAAAGTATCCATCCCTTACAGCTGAAGAGAGAACTGATGAAGCTGG 306

OY 353 CTGCCCCAAAGAGATCAGACGCCGCCCTTCATCTTTATAGGGCTCAGGTGGCTCCT 412
DB 305 CTGCCCCAAAGAGATCAGACGCCGCCCTTCATCTTTATAGGGCTCAGGTGGCTCCT 246

OY 413 GGAACATGCTGGAGTGGGGGCTCAACCCGAGTGGTTTCATCTGACCTCTCCATTTGTA 472

```

```

DB 245 GGAACATGCTGGAGTGGGGGCTCAACCCGAGTGGTTTCATCTGACCTCTCCATTTGTA 186
OY 473 ATGAGCTGTGGGGTGAAGATTAATTGGAACAGCAAGCAACATGATTTGATTTTC 532
DB 185 ATGAGCTGTGGGGTGAAGATTAATTGGAACAGCAAGCAACATGATTTGATTTTC 126

OY 533 AACCACTTTCGCAAAAGCTGAAATGAGCCCGAGTGAAGTCAAGCATTTAG 579
DB 125 AACCACTTTCGCAAAAGCTGAAATGAGCCCGAGTGAAGTCAAGCATTTAG 79

RESULT 4
AO041691/c 316 bp DNA linear GSS 14-JUL-1998
LOCUS CIT-HSP-2326018.TR CIT-HSP Homo sapiens genomic clone 2326018, DNA
DEFINITION sequence.
ACCESSION AO041691
VERSION AO041691.1 GI:3310962
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 316)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wblle,C., Shizuya,H.,
Simon,M. and Venter,J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
JOURNAL Unpublished (1998)
COMMENT Other_GSSs: CIT-HSP-2326018.TV
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
FEATURES
source
1. .316
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2326018"
/clone_lib="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBeloBAC11; Site.1: HindIII; Site.2:
HindIII"
BASE COUNT 79 a 70 c 75 g 89 t 3 others
ORIGIN
Query Match 38.6%; Score 223.4; DB 17; Length 316;
Best Local Similarity 99.0%; Pred. No. 7.8e-54;
Matches 224; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 355 GCCCAAAAGATATGACAGCGCGCTTCATCTTTATAGGGCTCAGTGGCTCCTGG 414
DB 316 GCCCAAAAGATATGACAGCGCGCTTCATCTTTATAGGGCTCAGTGGCTCCTGG 257

OY 415 AACATGCTGAGTGGGGGCTCACCCGAGTGGTCAATGACACTCTGCAATTTGTAAT 474
DB 256 AACATGCTGAGTGGGGGCTCACCCGAGTGGTCAATGACACTCTGCAATTTGTAAT 197

OY 475 GAGCTGTGGGGTGAAGATTAATTGGAACAGCAAGCAACATGATTTGATTTGCA 534
DB 196 GAGCTGTGGGGTGAAGATTAATTGGAACAGCAAGCAACATGATTTGATTTGCA 137

OY 535 CCAGTTTGCAAAAGCTGAAATGAGCCCGAGTGAAGTCAAGCATTTAG 579

```

Db 136 CCAAGTTCGAAGTGAATGACCCGACGAGGAGGAGGATAG 92

RESULT 5

AK009787

LOCUS

1219 bp

mRNA

linear

HTC 19-JAN-2002

DEFINITION

Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310043N20;homolog to F111 E7A, full insert sequence.

ACCESSION

AK009787

VERSION

AK009787.1

GI:12844799

KEYWORDS

HTC; CAP trapper.

SOURCE

Mus musculus (strain:C57BL/6J) adult male tongue cDNA to mRNA, clone:lib:RIKEN full-length enriched mouse cDNA library

ORGANISM

Mus musculus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)

JOURNAL

99279253

MEDLINE

10349636

REFERENCE

2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL

20499374

MEDLINE

11042159

REFERENCE

3 Shibata, K., Itoh, M., Aizawa, K., Nagasaki, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunaka, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, K., Izawa, M., Ohara, E., Matabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A., and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multichipillary sequencer Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL

20530913

MEDLINE

11076861

REFERENCE

4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, K., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamataka, I., Saito, T., Okazaki, Y., Gojodori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleschmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L. M., Stabli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombert, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Welter, C., Whitaker, C., Wilmberg, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohlski, S. and Hayashizaki, Y. Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)

JOURNAL

21085660

MEDLINE

11217851

REFERENCE

5 (bases 1 to 1219)

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Atakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C.,

COMMENT

JOURNAL

10349636

REFERENCE

2 Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hirose, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koyama, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, K., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shitaki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toyama, M., Yamamura, T., Yamataka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Direct Substitution Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216) Please visit our web site (http://genome.gsc.riken.go.jp/) for further details. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5'] GAGAGAGAGATTCGACTTATTAATTAATCCCGCCCCCCC 3']. cDNA was prepared by using triazole thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot - 5.0 and subtraction to Rot - 25.0. Second strand cDNA was prepared with the primer adapter of sequence [5'] GAGAGAGATTCGACTTATTAATTAATCCCGCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI. Host: SOLR. Location/Qualifiers 1..1219 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="FANTOM_DB:2310043N20" /db_xref="MGI:1901829" /db_xref="MGI:1901829" /db_xref="taxon:10090" /clone="2310043N20" /sex="male" /tissue_type="tongue" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="adult" 78..629 /note="data source:SPRR, source key:Q9UHA5, evidence:ISS homolog to F111 E7A putative" /codon_start=1 /protein_id="BAB26505.1" /db_xref="GI:12844800" /db_xref="MGI:1916927" /translation="MMAFPQSCVAVLPKSIOMEPNHTMHSSQSPRYRHDSQ EWAVVLTGNTLAVPANNVKKVILSLACDTEPDQVKKLVFLGIRKNLCCFCV EMEGKPTDLKEVDIMNLYKKKAKAPLFLHNGIESISVQSVLYGWFATSISSIER OTTILTHNGKLVNTNFTIESK" 1199..1204 /note="putative" 1219 /note="putative" BASE COUNT 380 a 272 c 217 g 350 t ORIGIN Query Match 8.8%; Score 51.2; DB 11; Length 1219; Best Local Similarity 48.6%; Pred. No. 0.00092; Matches 236; Conservative 0; Mismatches 238; Indels 12; Gaps 3; 91 CCGAGAGATTCGACTTATTAATTAATCCCGCCCCCCC 150

Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashtivagi, K., Yukiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Inoue, Y., Kikita, T., Matsuura, S., Kawai, J., Ozazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashiizaki, Y.

TITLE
RIKEN Integrated sequence analysis (RISA) system—384-format
sequencing pipeline with 384 multichannel sequencer

JOURNAL
Genome Res. 10 (11), 1757-1771 (2000)

	REFERENCE	2	Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M. and Hayashizaki Y.
AUTHORS	TITLE		Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL MEDLINE	PUBMED	20499374	Genome Res. 10 (10), 1617-1630 (2000)
REFERENCE	AUTHORS	3	Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsuna T., Tashiro H., Itoh M., Suni N., Ishii Y., Nakamura S., Hazama N., Nishino T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe Y., Yoneda Y., Ishikawa T., Ozawa Y., Tanaka T., Matsura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kita A. and Hayashizaki Y.
JOURNAL MEDLINE	PUBMED	11042159	Riken integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipipillary sequencer
REFERENCE	AUTHORS	4	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H., Ashburner M., Batalov S., Casavant T., Fleischmann N.W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Strabli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Anou H., Baldarelli R., Barsh G., Blake J., Boftelli D., Bolunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hotmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch R.F., Suzuki H., Toyok Oka K., Wang R.H., Weitz C., Whitaker C., Wilting L., Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S. and Hayashizaki Y.
JOURNAL MEDLINE	PUBMED	21085660	Functional annotation of a full-length mouse cDNA collection
REFERENCE	AUTHORS	5	(bases 1 to 1531) Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A., Arikawa T., Baldarelli R., Bono H., Brownstein M., Bull C., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanagaki T., Hara A., Hayatsu N., Hill D., Hiramoto K., Hiroaka T., Hori F., Hume D., Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H., Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ono M., Okazaki Y., Okido T., Owa C., Quackenbush J., Saito H., Saito R., Sakai K., Sakai K., Sano H., Sasaki D., Schriml L., Shibata K., Shibata Y., Shingawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toyota T., Yamamura T., Yamakawa I., Yasunishi A., Yoshida K., Yoshino M., Muramatsu M. and Hayashizaki Y.
JOURNAL MEDLINE	PUBMED	11217851	Direct Submission Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-test@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT			Please visit our web site (http://genome.gsc.riken.go.jp/) for further details. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGGAGGAGGAGGATCCGACGAGCTCTTTTCTTTTCTTNN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap tripper. cDNA went through one round of normalization to Rot = 5.0 and subtraction to Rot = 25.0. Second strand cDNA was prepared with the primer adapter of sequence [3' GAGGAGGAGGATTCGAGTAAATTAATTAATTCGCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI. Host: SOLR.

```

FEATURES
source
    Location/Qualifiers
    1..1531
    /organism="Mus musculus"
    /strain="C57BL/6J"
    /db_xref="FANTOM_DB:2310063B08"
    /db_xref="MGD:MGI:1898160"
    /db_xref="taxon:10090"
    /clone="2310063B08"
    /sex="male"
    /tissue_type="tongue"
    /clone_lib="RIKEN full-length enriched mouse cDNA library"
    /dev_stage="adult"
    1..1531
    /gene="Irf15"
    1..1531
    /gene="Irf15"
    /note="data source:MGD, source key:MGI:1859325,
evidence:ISS
interleukin 1 family, member 5 (delta)"
    /db_xref="MGD:MGI:1859325"
BASE COUNT      393 a      367 c      368 g      403 t
ORIGIN

```

Query Match	7.08;	Score 40.6;	DB 11;	Length 1531;
Best Local Similarity	57.58;	Pred. No. 1.2;		
Matches 73; Conservative	0;	Mismatches 54;	Indels 0;	Gaps 0;

QY	381	CTTCACATCTTTTATAGAGGCTCAGAGGGGCTCTCTGAGACATGCTGAGATCGGCGGGCTACC	44.0
Db	517	CTTCACACTTCACGCGGGGAAATGAGTCTTACCTCCAGACTTCGAATCCGGTGGCTACC	57.6
QY	441	CGGATGGTCACTCAGCTCAGCTCTCATTTATATGAGCCTGTGGGGGACAGATAATT	50.0
Db	577	AGGCTGGTTCCTCTGCACTACCGGAACTGACACGCTTGACGGCTCACTCAAGATCC	63.6
QY	501	TCGAGAAC	50.7
Db	637	TCGAGAAC	64.3

RESULT 10	LOCUS	DEFINITION
AK014576	AK014576	2843 bp mRNA linear HTC 19-2AN-2002 Mus musculus 0 day neonate skin CDNA, RIKEN full-length enriched library, clone:4632413M13:interleukin 1 family, member 5 (delta), full insert sequence.

ACCESSION	AK014576
VERSION	AK014576.1
KEYWORDS	GI:12852516
SOURCE	HTC; CAP trapper.
	Mus musculus (Strain:C57BL/6J) 0 day neonate skin cDNA to mRNA,
	clone_lib:RIKEN full-length enriched mouse cDNA library
	clone:6532413N13.
ORGANISM	Mus musculus

Eumaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

REFERENCE	1
AUTHORS	Carinanci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99219253
PUBMED	10349636
REFERENCE	2

Brazil
Rua Flv. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP.
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following way:

(http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC1&t2=RC1-CT0251-141099-012-c02&t3=1999-10-14&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 35

High quality sequence stop: 436.

FEATURES

source

Location/Qualifiers

1. 436

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone.lib="CT0251"

/dev_stage="Adult"

/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196

716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

BASE COUNT

123 a 96 c 103 g 114 t

ORIGIN

Query Match 6.5%; Score 37.8; DB 10; Length 436;

Best Local Similarity 52.1%; Pred. No. 5.2; Mismatches 117; Indels 6; Gaps 2;

Matches 134; Conservative 0; Mismatches 117; Indels 6; Gaps 2;

QY 295 GATAAAGGACAAAGTCATCCCTTCAGCTGAAGAAGAACTGATGAGCTGCT 354

DB 430 GAGAAAGTTGGAGAACACCCACATTCAGCTAAAGAGCAAGATCATGATCTTAT 371

QY 355 GCCCAAAAGAAATCAGACGCCGCCCTTCATCTTTATAGGGCTCAGGTGGCTCTGG 414

DB 370 GGCACACCCGAGCCCG--TGAAACCCCTCTCTTTTACCGTCCAGAGCTGTAGAGCC 314

QY 415 AACATGCTGGAGTGGGGGCTCACCCGATGCTTCATCTGACCTCTCGAATTGTAT 474

DB 313 TCACACCTTGATCTGTGGCTCTCCCGACGTGTTCA--TGCCTCTCCAAAGAGAGAC 257

QY 475 GAGCCTGTGGGGTGACAGATAATTGAGAGCAAGAAACATGATTTTCATTCAA 534

DB 256 CAGCCCATCATCTTCGACTTCAGAACTTGGAGATACACACACTGCCCTTGCAGTAAT 197

QY 535 CCAAGTTGCAAGCTGA 551

DB 196 ATTAATGACTGAACCTCA 180

RESULT 14

AM368430 539 bp mRNA linear EST 04-FEB-2000

LOCUS CM3-HT0192-071099-022-e12 HT0192 Homo sapiens cDNA, mRNA sequence.

DEFINITION AM368430

ACCESSION AM368430.1 GI:6873080

VERSION EST.

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 539)

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE HGP http://www.ludwig.org.br/ORESTES.

JOURNAL The FAPESP/LICR Human Cancer Genome Project

COMMENT Unpublished (1999)

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?l=CM3&t2=CM3-HT0192-

071099-022-e12&t3=1999-10-07&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 21

High quality sequence stop: 539.

FEATURES

source

Location/Qualifiers

1. 539

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone.lib="HT0192"

/dev_stage="Adult"

/note="Organ: head-neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the puc 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

BASE COUNT

145 a 131 c 123 g 140 t

ORIGIN

Query Match 6.5%; Score 37.8; DB 10; Length 539;

Best Local Similarity 52.1%; Pred. No. 5.6; Mismatches 117; Indels 6; Gaps 2;

Matches 134; Conservative 0; Mismatches 117; Indels 6; Gaps 2;

QY 295 GATAAAGGACAAAGTCATCCCTTCAGCTGAAGAAGAACTGATGAGCTGCT 354

DB 533 GAGAAAGTTGGAGAACACCCACATTCAGCTAAAGAGCAAGATCATGATCTTAT 474

QY 355 GCCCAAAAGAAATCAGACGCCGCCCTTCATCTTTATAGGGCTCAGGTGGCTCTGG 414

DB 473 GGCACACCCGAGCCCG--TGAAACCCCTCTCTTTTACCGTCCAGAGCTGTAGAGCC 417

QY 415 AACATGCTGGAGTGGGGGCTCACCCGATGCTTCATCTGACCTCTCGAATTGTAT 474

DB 416 TCACACCTTGATCTGTGGCTCTCCCGACGTGTTCA--TGCCTCTCCAAAGAGAGC 360

QY 475 GAGCCTGTGGGGTGACAGATAATTGAGAGCAAGAAACATGATTTTCATTCAA 534

DB 359 CAGCCCATCATCTTCGACTTCAGAACTTGGAGATACACACACTGCCCTTGAATTAAT 300

QY 535 CCAAGTTGCAAGCTGA 551

DB 299 ATTAATGACTGAACCTCA 283

RESULT 15

AM361172 555 bp mRNA linear EST 04-FEB-2000

LOCUS RCI-CT0251-141099-012-h04 CT0251 Homo sapiens cDNA, mRNA sequence.

DEFINITION AM361172

ACCESSION AM361172.1 GI:6865822

VERSION EST.

KEYWORDS human.

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 555)

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE HGP http://www.ludwig.org.br/ORESTES.

JOURNAL The FAPESP/LICR Human Cancer Genome Project

COMMENT Unpublished (1999)

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC1&t2=RC1-CT0251-

141099-012-h04&t3=1999-10-14&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 555.

FEATURES

Source

Location/Qualifiers

1.555

```
/organism="Homo sapiens"  
/db xref="taxon:9606"
```

/db xref="taxon:9606"

```
/clone_lib="CT0251"
```

```
/clone_lib="CT0251"
```

```
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
```

from ORESTES PCR (U.S. Letters Patent application No. 1965

ORESTES PCR (U.S. Letters Patent application No. 196

716 - Ludwig Institute for Cancer Research) profiles

into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low

mRNA and cDNA amplification were performed under low

stringency conditions. "

BASE COUNT	148 a	129 c	130 g	147 t	1 others
ORIGIN					

ORIGIN

Query Match	6.58;	Score 37.8;	DB 10;	Length 555;
Query Match	6.58;	Score 37.8;	DB 10;	Length 555;

Best Local Similarity 52.18; Pred. No. 5.67;

Matches 134; Conservative 0; Mismatches 117; Indels 6; Gaps 2;

295 GATAAGGACAAAGTCATCCCTTCAGCTGAAGGAAGGAGAACTGATGAAGCTGGCT 354

Db 7 GAGAAGTTGGAGACAGCCACATTCGACCTAAAAGAGCAGAAGATCATGGATCTGTAT 66

355 GCCCAAAGGATCAGCAGCGCCCTTCATCTTTATAGGCTCAGGTGGCTCCTGG 414

Db 67 GGCACCCGAGCCG---TGAACCTTCTCTACCGTGCCAGACTGTAGGACC 123

415 AACATGCTGAGTCGGGGCTCACC CGATGTT CATCTGCACCTCCTGCAATGTAAT 474

Db 124 TCCACCCCTGAGTCTGTGGCCTTCCCGACTGGTTCAT--TGCCCTCCCAAGAGAGAC 180

QY 475 GAGCCTGTGGGTGACAGATAAATTGAGAACAGGAACACATTTGAATTTTCATTCAA 534

Db 181 CAGCCCATCTTCTGACTTCAGACTTGGGAGTCATACAACTGCGCTTGAAATTAAT 240

QY 535 CCAGTTTGCAAGCTGA 551

Db 241 ATAAATGACTGAACCTCA 257

Search completed: May 3, 2003, 06:28:04
Job time : 1511 secs

Job time : 1511 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2003, 06:28:12 ; Search time 92 Seconds
(without alignments)
278.088 Million cell updates/sec

Title: US-09-876-790-3

Perfect score: 1017
Sequence: 1 MSGCDRRETETGKNSFKK.....IEFSPQVCKAMSPSEVSD 192

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A.GeneSeq_101002:*

- 1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
- 2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
- 5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
- 6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
- 7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
- 8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
- 9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
- 10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
- 11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
- 12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
- 13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
- 14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
- 15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
- 16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
- 17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
- 18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
- 19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1017	100.0	192	21	AAV95297 Human interleukin-
2	906	89.1	203	21	AAV96933 Human IL-1R1a fuse
3	905	89.0	197	21	AAV95300 Human interleukin-
4	895	88.0	198	22	AAAB85138 Interleukin-1 homo
5	895	88.0	207	21	AAV96938 Human IL-1 recepto
6	895	88.0	218	21	AAAB28266 Human interleukin-
7	895	88.0	218	21	AAV96940 Human IL-1 recepto
8	895	88.0	218	21	AAV70927 Human zilla4 prote
9	895	88.0	218	21	AAV95299 Human interleukin-
10	895	88.0	218	21	AAV91885 Primate interleuki

11	895	88.0	218	22	AAAG68116 Human interleukin
12	895	88.0	218	22	AAAB85136 Interleukin-1 homo
13	895	88.0	218	22	AAAB47186 IL-1 related polyP
14	892	87.7	218	21	AAV71084 Human zilla4-E200D
15	891	87.6	218	21	AAV70933 Human zilla4-E200K
16	885	87.0	193	21	AAV96934 Processed human IL
17	885	87.0	193	22	AAAB87596 Human PRO3435. Ho
18	883	86.8	167	21	AAV96932 Human IL-1 recepto
19	883	86.8	176	22	AAAB48081 Human extracellular
20	879	86.4	218	21	AAV70931 Human zilla4 varia
21	864	85.0	163	21	AAV97069 Human IL-1 recepto
22	859	84.5	218	21	AAV91884 Primate interleuki
23	775	76.2	218	21	AAV70928 Human zilla4 varia
24	704	69.2	167	21	AAV96939 Human IL-1 recepto
25	702	69.0	167	20	AAW93060 Human Tango-77 pro
26	702	69.0	178	20	AAW93057 Human Tango-77 pro
27	695	68.3	136	20	AAW93063 Human zilla4 splic
28	688	67.6	157	21	AAV70929 Human interleukin-
29	688	67.6	157	21	AAV95301 Human zilla4 varia
30	684	67.3	157	21	AAV70934 Human zilla4 varia
31	672	66.1	157	21	AAV70932 Human Tango-77 pro
32	623	61.3	115	20	AAW93059 Human Tango-77 mat
33	623	61.3	115	20	AAW93065 Human Tango-77 mat
34	618	60.8	114	20	AAW93062 Human IL-1 recepto
35	596	58.6	110	21	AAV97066 Human IL-1 recepto
36	568	55.9	157	21	AAV70930 Human polypeptide
37	469	46.1	123	22	AAO04444 Human interleukin-
38	229	22.5	157	22	AAE04299 Human IL-1 eta. H
39	229	22.5	157	22	AAAB50444 Human interleukin-
40	229	22.5	170	22	AAAB85000 Human novel secret
41	226.5	22.3	172	22	AAE017010 Human gene 13 enco
42	226.5	22.3	172	22	AAE09702 Interleukin-1 rece
43	225.5	22.2	169	19	AAW63136 A human SPOTL-1 pr
44	225.5	22.2	169	20	AAV24043 Human interleukin-
45	225.5	22.2	169	20	AAV24395

ALIGNMENTS

RESULT 1
AAV95297
ID AAV95297 standard; Protein; 192 AA.
XX
AC AAV95297;
XX
DT 12-SEP-2000 (first entry)
XX
DE Human interleukin-1 zeta.
XX
KW Interleukin-1 zeta; IL-1 zeta; human; therapy; inflammation; fever.
XX
OS Homo sapiens.
XX
PN WO200036108-A2.
XX
PD 22-JUN-2000.
XX
PF 14-DEC-1999; 99WO-US29549.
XX
PR 14-DEC-1998; 98US-0112163.
PR 10-NOV-1999; 99US-0164675.
XX
PA (IMMUNEX CORP.
XX
PI Sims JE, Smith DE, Born TL;
XX
DR WPI; 2000-442387/38.
DR N-PSDB; AAA27918.
XX
PT Isolated interleukin-1 (IL-1) zeta nucleic acids and splice variants
PT TDZ1, TDZ2, TDZ3 and their encoding proteins, useful as probes for
PT identifying genes associated with diseases such as glaucoma, and

```

PT Insulin-dependent diabetes mellitus
XX
PS Claim 10; Page 8; 87pp; English.
XX
CC The present sequence is that of human interleukin-1 zeta (IL-1
CC zeta), a member of the IL-1 family. The sequence was determined
CC by translation of the nucleotide sequence of isolated IL-1 zeta
CC cDNA (see AAA27918). IL-1 zeta mRNA is generated from exons 3-6 of
CC the IL-1 zeta locus. The mRNA is expressed most strongly in the
CC testis, prostate, colon, brain, placenta, lung, foetal liver and
CC lymph node stroma, lung, testis and placenta. The invention is
CC directed to novel, purified and isolated IL-1 zeta, IL-1 zeta
CC splice variants and Xrec2 polypeptides (see AAY95297-301), the
CC nucleic acids (see AAA27918-22) encoding such polypeptides, processes
CC for production of recombinant forms of such polypeptides, and
CC their uses. The polypeptides can be used to study cellular
CC processes such as immune regulation, cell proliferation, cell
CC death, cell migration, cell-to-cell interaction and inflammatory
CC responses, to identify proteins associated with IL-1 zeta, to
CC screen for potential inhibitors, and to prepare antibodies. In
CC particular, they can be used to activate and/or inhibit the
CC activation of vascular endothelial cells and lymphocytes, induce
CC and/or inhibit the induction of local tissue destruction and fever,
CC inhibit and/or stimulate macrophages and vascular endothelial cells
CC to produce IL-6, induce and/or inhibit the induction of
CC prostaglandins, nitric oxide synthetase, and metalloproteases, and
CC upregulate and/or inhibit the upregulation of molecules on the
CC surface of vascular endothelial cells.
XX
SQ Sequence 192 AA;
XX
Query Match 100.0%; Score 1017; DB 21; Length 192;
Best Local Similarity 100.0%; Pred No. 5,6e-111;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MSGCDRRETEFKGNSEFKRLGKPKYKNLNPKRFSIHDDHKVLDVDSGNLAVDPKNYI 60
DB 1 MSGCDRRETEFKGNSEFKRLGKPKYKNLNPKRFSIHDDHKVLDVDSGNLAVDPKNYI 60
OY 61 RPEIFALASSLSASAEGKSPILIGVSKGEFLCYCDKDGSHPSLQKKELMKMLAAQ 120
DB 61 RPEIFALASSLSASAEGKSPILIGVSKGEFLCYCDKDGSHPSLQKKELMKMLAAQ 120
OY 121 KESARRPFIIFYRAQVGSNMNLESNAHGWFTICTSCNNEPVGYTDFENRKHIEFSFQPV 180
DB 121 KESARRPFIIFYRAQVGSNMNLESNAHGWFTICTSCNNEPVGYTDFENRKHIEFSFQPV 180
OY 181 CKAEMSPSEVSD 192
DB 181 CKAEMSPSEVSD 192
XX
RESULT 2
AAY96933
ID AAY96933 standard; Protein; 203 AA.
XX
AC AAY96933;
XX
DT 31-OCT-2000 (first entry)
XX
DE Human IL-1RA1 fused to heterologous signal sequence.
XX
KW hIL-1RA1; human interleukin-1 receptor antagonist-1; IL-1IP; osteopathic;
KW interleukin-1-like polypeptide; anti-inflammatory; anti-asthmatic;
KW anti-arthritis; antimicrobial; respiratory; anti-ischemic; vaccine;
KW dermatological; immunomodulatory; gastrointestinal; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..15
FT /Label= Signal_peptide
FT Peptide 16..23

```

```

FT /Label= Flag-tag
FT Peptide 24..36
FT /Label= Linker
FT Protein 37..203
FT /Label= hIL-1RA1
XX
XX W0200039297-A2.
XX
XX 06-JUL-2000.
XX
XX 22-DEC-1999; 99MO-US30720.
XX
XX 23-DEC-1998; 98US-0113430.
XX 22-JAN-1999; 99US-0116843.
XX 13-APR-1999; 99US-0129122.
XX
XX (GETH ) GENENTECH INC.
XX
XX Goddard A, Pan J;
XX
XX WPI; 2000-452395/39.
XX N-PSDB; AAA51592.
XX
XX Nucleic acids encoding interleukin-1-like polypeptides, useful for
XX preventing and treating e.g. inflammation, asthma and psoriasis
XX
XX Claim 22; Fig 2; 143pp; English.
XX
XX An isolated nucleic acid molecule encoding an interleukin-1-like
XX polypeptide (IL-1IP) that retains one or more activities of the peptide
XX from which it is derived, such as the IL-1RA1 binding activity of a human
XX interleukin-1 receptor antagonist-1 (hIL-1RA1) polypeptide, is new. The
XX nucleic acids may be used in molecular engineering applications, e.g.
XX hybridization assays and chromosome and gene mapping studies, for
XX recombinantly producing the IL-1IP polypeptide or for producing gene
XX knock out animals to study the role of the protein in metabolism and
XX disease processes (conversely, gene therapy protocols may be used to
XX supplement a patient's production of the polypeptide or to rectify
XX mutations that lead to the production of in active peptides). The
XX peptides produced may be used to screen for and produce modulators (e.g.
XX antibodies) of IL-1IP protein expression and activity which may be use
XX to treat disorders associated with inappropriate IL-1IP expression and
XX activity, such as inflammatory disorders, asthma, arthritis,
XX osteoarthritis, sepsis, acute lung injury, adult respiratory distress
XX syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
XX psoriasis, graft versus host disease and/or inflammatory bowel disease.
XX
XX Sequence 203 AA;
XX
Query Match 89.1%; Score 906; DB 21; Length 203;
Best Local Similarity 100.0%; Pred. No. 6,8e-98;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 22 RGRVKVKNLNPKRFSIHDDHKVLDVDSGNLAVDPKNYIRPEIFALASSLSASAEGS 81
DB 22 RGRVKVKNLNPKRFSIHDDHKVLDVDSGNLAVDPKNYIRPEIFALASSLSASAEGS 81
OY 82 PILLGVSKGEFLCYCDKDGSHPSLQKKELMKMLAAKESARRPFIIFYRAQVGSNMML 141
DB 82 PILLGVSKGEFLCYCDKDGSHPSLQKKELMKMLAAKESARRPFIIFYRAQVGSNMML 141
OY 93 PILLGVSKGEFLCYCDKDGSHPSLQKKELMKMLAAKESARRPFIIFYRAQVGSNMML 152
DB 93 PILLGVSKGEFLCYCDKDGSHPSLQKKELMKMLAAKESARRPFIIFYRAQVGSNMML 152
OY 142 ESAAHGWFICTSCNNEPVGYTDFENRKHIEFSFQPVCKAEMSPSEVSD 192
DB 142 ESAAHGWFICTSCNNEPVGYTDFENRKHIEFSFQPVCKAEMSPSEVSD 192
OY 153 ESAAHGWFICTSCNNEPVGYTDFENRKHIEFSFQPVCKAEMSPSEVSD 203
DB 153 ESAAHGWFICTSCNNEPVGYTDFENRKHIEFSFQPVCKAEMSPSEVSD 203
XX
RESULT 3
AAY95300
ID AAY95300 standard; Protein; 197 AA.
XX
AC AAY95300;
XX
DT 12-SEP-2000 (first entry)

```

XX Human interleukin-1 zeta splice variant TDZ.2.
DE
XX

KM Interleukin-1 zeta; IL-1 zeta; splice variant; human; TDZ.2;
KM testis-derived zeta variant; therapy; inflammation; fever.
XX
XX

OS Homo sapiens.

PN WO200036108-A2.

XX 22-JUN-2000.

PD 14-DEC-1999; 99WO-US29549.

XX 14-DEC-1998; 98US-0112163.

PR 10-NOV-1999; 99US-0164675.

XX (IMMV) IMMUNEX CORP.

PI Sims JE, Smith DE, Born TL;

XX WPI: 2000-442387/38.

DR N-PSDB; AAA27921.

XX Isolated interleukin-1 (IL-1) zeta nucleic acids and splice variants
PT TDZ1, TDZ2, TDZ3 and their encoding proteins, useful as probes for
PT identifying genes associated with diseases such as glaucoma, and
PT insulin-dependent diabetes mellitus -

XX Claim 10; Page 11; 87pp; English.

XX The present sequence is that of splice variant TDZ.2 (testis-derived
CC zeta variant) of human interleukin-1 zeta (IL-1 zeta). TDZ.2 mRNA
CC is generated from exons 1, 4, 5 and 6 of the IL-1 zeta locus, and
CC the encoded protein is probably a functional IL-1 like molecule.
CC TDZ.2 mRNA is expressed most strongly in the testis and bone marrow.
CC The invention is directed to novel, purified and isolated IL-1
CC zeta, its splice variants and Xrec2 polypeptides (see AAY95297-301),
CC the nucleic acids (see AAA27918-22) encoding such polypeptides,
CC processes for production of recombinant forms of such polypeptides,
CC and their uses. The polypeptides can be used to study cellular
CC processes such as immune regulation, cell proliferation, cell
CC death, cell migration, cell-to-cell interaction and inflammatory
CC responses, to identify proteins associated with IL-1 zeta, to
CC screen for potential inhibitors, and to prepare antibodies. In
CC particular, they can be used to activate and/or inhibit the
CC activation of vascular endothelial cells and lymphocytes, induce
CC and/or inhibit the induction of local tissue destruction and fever,
CC inhibit and/or stimulate macrophages and vascular endothelial cells
CC to produce IL-6, induce and/or inhibit the induction of
CC prostaglandins, nitric oxide synthetase, and metalloproteases, and
CC upregulate and/or inhibit the upregulation of molecules on the
CC surface of vascular endothelial cells.
XX

SO Sequence 197 AA;

Query Match 89.0%; Score 905; DB 21; Length 197;
Best Local Similarity 99.4%; Pred. No. 8.5e-98;
Matches 171; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 LRGRKVNLPKRFSSIHDDHKLVLVDSGNLIAVPDKNTIRPELFFALASSLSASAEKG 80
DB 26 LGRKVNLPKRFSSIHDDHKLVLVDSGNLIAVPDKNTIRPELFFALASSLSASAEKG 85
QY 81 SPILGVSKEGFCILYCDKDGSGSHPSLOLKKRKLMLAAOKESARRPFIYRAOVGSWMN 140
DB 86 SPILGVSKEGFCILYCDKDGSGSHPSLOLKKRKLMLAAOKESARRPFIYRAOVGSWMN 145
QY 141 LESAAHGMFICTSCNCEPVGVTDFENRKHIEFSFQPVCKAEMSPSEVSD 192
DB 146 LESAAHGMFICTSCNCEPVGVTDFENRKHIEFSFQPVCKAEMSPSEVSD 197

RESULT 4

AA885138
ID AAB85138 standard; Protein; 198 AA.

XX AAB85138;

AC 22-AUG-2001 (first entry)

XX Interleukin-1 homologue (IL-1H4) mature polypeptide.

DE Interleukin-1; IL-1H4; antiinflammatory; antibacterial; antiallergic;
XX immunosuppressive; antipruritic; antiarthritic; cytostatic; antiHIV;
XX cerebroprotective; antiaesthetic; vasodilator; osteopathic;
KM immunostimulant; antiarteriosclerotic; nootropic; neuroprotective;
XX gene therapy; vaccine.

XX Homo sapiens.

OS WO200140247-A1.

XX 07-JUN-2001.

PD 30-NOV-2000; 2000WO-US32521.

XX 01-DEC-1999; 99US-0452140.

XX (SMK) SMITHKLINE BEECHAM CORP.

XX Kumar S, McDonnell PC, Young PR;

XX WPI: 2001-369949/41.

XX Novel Interleukin-1 homologue, IL-1H4, for treating chronic and acute
PT inflammation, septicemia, autoimmune diseases, transplant rejection,
PT graft versus host disease, stroke, ischemia, allergy and asthma -

XX Claim 1; Page 29; 30pp; English.

XX The invention provides an isolated interleukin-1 homologue, IL-1H4
CC polypeptide. The IL-1H4 polypeptide can be expressed by standard
CC recombinant methodology. The IL-1H4 polypeptide, polynucleotides and
CC modulators are useful for treating chronic and acute inflammation,
CC septicemia, autoimmune diseases (e.g., inflammatory bowel disease,
CC psoriasis and arthritis), transplant rejection, graft versus host
CC disease, infection, stroke, ischemia, acute respiratory disease syndrome,
CC allergies, asthma, restenosis, brain injury, AIDS, bone diseases (e.g.,
CC osteoporosis), cancer (e.g., lymphoproliferative disorders), congestive
CC heart failure, atherosclerosis and Alzheimer's disease. The IL-1H4
CC polynucleotides are useful as diagnostic reagents and for chromosome
CC identification. The present sequence represents the IL-1H4 mature
CC polypeptide.
XX

SO Sequence 198 AA;

Query Match 88.0%; Score 895; DB 22; Length 198;
Best Local Similarity 100.0%; Pred. No. 1.3e-96;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 PKYKLNLPKRFSSIHDDHKLVLVDSGNLIAVPDKNTIRPELFFALASSLSASAEKGSPT 83
DB 30 PKYKLNLPKRFSSIHDDHKLVLVDSGNLIAVPDKNTIRPELFFALASSLSASAEKGSPT 89
QY 84 LIGVSGEGCICVCDKDGSGSHPSLOLKKRKLMLAAOKESARRPFIYRAOVGSWMN 143
DB 90 LIGVSGEGCICVCDKDGSGSHPSLOLKKRKLMLAAOKESARRPFIYRAOVGSWMN 149
QY 144 AAHPGMFICTSCNCEPVGVTDFENRKHIEFSFQPVCKAEMSPSEVSD 192
DB 150 AAHPGMFICTSCNCEPVGVTDFENRKHIEFSFQPVCKAEMSPSEVSD 198

RESULT 5
AA196938

ID AAY6938 standard; Protein: 207 AA.
XX
AC AAY6938;
XX
DT 31-OCT-2000 (first entry)
XX
DE Human IL-1 receptor antagonist 1 long.
XX
KW hIL-1raIL; human interleukin-1 receptor antagonist-1 long; IL-11p;
KW osteopathic; interleukin-1-like polypeptide; anti-inflammatory;
KW anti-asthmatic; anti-arthritic; antimicrobial; respiratory; vaccine;
KW anti-ischemic; dermatological; immunomodulatory; gastrointestinal;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN WO200039297-A2.
XX
PD 06-JUL-2000.
XX
PF 22-DEC-1999; 99WO-US30720.
XX
PR 23-DEC-1998; 98US-0113430.
PR 22-JAN-1999; 99US-0116843.
PR 13-APR-1999; 99US-0129122.
XX
PA (GETH) GENENTECH INC.
XX
PI Goddard A, Pan J;
XX
DR WPI: 2000-452395/39.
DR N-PSDB: AAA51601.
XX
PT Nucleic acids encoding interleukin-1-like polypeptides, useful for
PT preventing and treating e.g. inflammation, asthma and psoriasis
XX
PS Claim 22; Fig 15; 143pp; English.
XX
CC An isolated nucleic acid molecule encoding an interleukin-1-like
CC polypeptide (IL-11p) that retains one or more activities of the peptide
CC from which it is derived, such as the IL-18R binding activity of a human
CC interleukin-1 receptor antagonist-1 (hIL-1ra1) polypeptide, is new. The
CC nucleic acids may be used in molecular engineering applications, e.g.
CC hybridization assays and chromosome and gene mapping studies, for
CC recombinantly producing the IL-11p polypeptide or for producing gene
CC knock out animals to study the role of the protein in metabolism and
CC disease processes (conversely, gene therapy protocols may be used to
CC supplement a patient's production of the polypeptide or to rectify
CC mutations that lead to the production of in active peptides). The
CC peptides produced may be used to screen for and produce modulators (e.g.
CC antibodies) of IL-11p protein expression and activity which may be use
CC to treat disorders associated with inappropriate IL-11p expression and
CC activity, such as inflammatory disorders, asthma, arthritis,
CC osteoarthritis, sepsis, acute lung injury, adult respiratory distress
CC syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
CC psoriasis, graft versus host disease and/or inflammatory bowel disease.
XX
SQ Sequence 207 AA:

Query Match 88.0%; Score 895; DB 21; Length 207;
Best Local Similarity 100.0%; Pred. No. 1.4e-96;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 159 AAHGWFTICSCNCPNPGVTDKFNKRKHIEFSQPVCRAKEMSPSEVSD 207
RESULT 6
AAB28266
ID AAB28266 standard; Protein: 218 AA.
XX
AC AAB28266;
XX
DT 13-FEB-2001 (first entry)
XX
DE Human interleukin-1 homologue IL-1H4.
XX
KW Human; interleukin-1 homologue; IL-1H4; inflammation; septicemia;
KW autoimmune disease; inflammatory bowel disease; psoriasis; arthritis;
KW transplant rejection; graft versus host disease; infection; stroke;
KW ischaemia; acute respiratory disease; allergy; asthma; restenosis;
KW brain injury; ARDS; bone disease; osteoporosis; cancer;
KW congestive heart failure; atherosclerosis; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO200063226-A1.
XX
PD 26-OCT-2000.
XX
PF 14-APR-2000; 2000WO-US10207.
XX
PR 16-APR-1999; 99US-0293625.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Young PR, McDonnell PC;
XX
DR WPI: 2000-687155/67.
DR N-PSDB: AAC66727.
XX
PT Interleukin-1 homolog useful for treating conditions such as chronic
PT and acute inflammation, septicemia, autoimmune diseases ischemia, acute
PT respiratory disease, allergies, and asthma -
XX
PS Claim 1; Pages 28-29; 30pp; English.
XX
CC The present sequence is human interleukin-1 homologue (IL-1H4). IL-1H4 is
CC useful for treating conditions such as chronic and acute inflammation,
CC septicemia, autoimmune diseases (e.g. inflammatory bowel disease,
CC psoriasis, and arthritis), transplant rejection, graft versus host
CC disease, infection, stroke, ischaemia, acute respiratory disease,
CC allergies, asthma, restenosis, brain injury, AIDS, bone diseases (e.g.
CC osteoporosis), cancer, congestive heart failure, atherosclerosis, and
CC Alzheimer's disease, related to either an excess of, or an
CC under-expression of, IL-1H4 polypeptide activity.
XX
SQ Sequence 218 AA:

Query Match 88.0%; Score 895; DB 21; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 PKVNLNPKKFSIHDDQHKVLYLDSGNLIVAPDKNYIRPEIFALASSLSASAEGSP1 83
DB 50 PKVNLNPKKFSIHDDQHKVLYLDSGNLIVAPDKNYIRPEIFALASSLSASAEGSP1 109
QY 84 LLGVSKEGFCYCDKDGSHPSLQKKEKIMKLAOKESARPPFIYRAOVGSMMNLES 143
DB 110 LLGVSKEGFCYCDKDGSHPSLQKKEKIMKLAOKESARPPFIYRAOVGSMMNLES 169
QY 144 AAHGWFTICSCNCPNPGVTDKFNKRKHIEFSQPVCRAKEMSPSEVSD 192
DB 170 AAHGWFTICSCNCPNPGVTDKFNKRKHIEFSQPVCRAKEMSPSEVSD 218

RESULT 7

AAV96940
 ID AAV96940 standard; Protein; 218 AA.
 XX
 AC AAV96940;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE Human IL-1 receptor antagonist 1 V.
 XX
 KW hIL-1RA1V; human interleukin-1 receptor antagonist-1; IL-1IP;
 KW osteopathic; interleukin-1-like polypeptide; anti-inflammatory;
 KW anti-asthmatic; anti-arthritis; antimicrobial; respiratory; vaccine;
 KW anti-ischemic; dermatological; immunomodulatory; gastrointestinal;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN MO200039297-A2.
 XX
 PD 06-JUL-2000.
 XX
 PE 22-DEC-1999; 99WO-US30720.
 XX
 PR 23-DEC-1998; 98US-0113430.
 PR 22-JAN-1999; 99US-0116843.
 PR 13-APR-1999; 99US-0129122.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Goddard A, Pan J;
 XX
 DR WPI: 2000-452395/39.
 DR N-PSDB; AAA51604.
 XX
 PT Nucleic acids encoding interleukin-1-like polypeptides, useful for
 PT preventing and treating e.g. inflammation, asthma and psoriasis
 XX
 PS Claim 22: Fig 19; 143pp; English.
 XX
 CC An isolated nucleic acid molecule encoding an interleukin-1-like
 CC polypeptide (IL-1IP) that retains one or more activities of the peptide
 CC from which it is derived, such as the IL-18R binding activity of a human
 CC interleukin-1 receptor antagonist-1 (hIL-1RA1) polypeptide, is new. The
 CC nucleic acids may be used in molecular engineering applications, e.g.
 CC hybridization assays and chromosome and gene mapping studies, for
 CC recombinantly producing the IL-1IP polypeptide or for producing gene
 CC knock out animals to study the role of the protein in metabolism and
 CC disease processes (conversely, gene therapy protocols may be used to
 CC supplement a patient's production of the polypeptide or to rectify
 CC mutations that lead to the production of an active peptides). The
 CC peptides produced may be used to screen for and produce modulators (e.g.
 CC antibodies) of IL-1IP protein expression and activity which may be use
 CC to treat disorders associated with inappropriate IL-1IP expression and
 CC activity, such as inflammatory disorders, asthma, arthritis,
 CC osteoarthritis, sepsis, acute lung injury, adult respiratory distress
 CC syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
 CC psoriasis, graft versus host disease and/or inflammatory bowel disease.
 XX
 SQ Sequence 218 AA;
 XX
 Query Match 88.0%; Score 895; DB 21; Length 218;
 Best Local Similarity 100.0%; Pred. No. 1.5e-96;
 Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 170 AAHPGFICTSCNCPNPGVTDKPFENRKHIETFPQVCKAEMSPSEVSD 218
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 RESULT 8
 AAV70927
 ID AAV70927 standard; Protein; 218 AA.
 XX
 AC AAV70927;
 XX
 DT 05-SEP-2000 (first entry)
 XX
 DE Human zilla4 protein.
 XX
 KW Human interleukin-1; IL-1; zilla4 protein; inflammation; arthritis;
 KW psoriasis; septic shock; graft-versus-host disease; leukaemia; cancer;
 KW anaemia; inflammatory bowel disease; acute neuropathology; shock;
 KW chronic neuropathology; respiratory disease syndrome; restenosis;
 KW acquired immune deficiency syndrome; AIDS; antiinflammatory; cytostatic;
 KW anti-arthritis; anti-psoriatic; antibacterial; immunosuppressive;
 KW anti-anaemic; neuroprotective; vasotropic;
 KW anti-human immunodeficiency virus; HIV.
 XX
 OS Homo sapiens.
 XX
 XX
 XX
 FT Key
 FT Domain
 FT /Label= Beta_strand
 FT 60..64
 FT /Label= Beta_strand
 FT 68..72
 FT /Label= Beta_strand
 FT 77..79
 FT /Label= Beta_strand
 FT 90..96
 FT /Label= Beta_strand
 FT 108..113
 FT /Label= Beta_strand
 FT 118..123
 FT /Label= Beta_strand
 FT 132..138
 FT /Label= Beta_strand
 FT 154..160
 FT /Label= Beta_strand
 FT 165..169
 FT /Label= Beta_strand
 FT 175..179
 FT /Label= Beta_strand
 FT 187..189
 FT /Label= Beta_strand
 FT 201..204
 FT /Label= Beta_strand
 FT 65..67
 FT /note= "Variable loop region involved in receptor
 FT binding"
 FT 73..76
 FT /note= "Variable loop region involved in receptor
 FT binding"
 FT 80..89
 FT /note= "Variable loop region involved in receptor
 FT binding"
 FT 97..107
 FT /note= "Variable loop region involved in receptor
 FT binding"
 FT 114..117
 FT /note= "Variable loop region involved in receptor
 FT binding"
 FT 124..131
 FT /note= "Variable loop region involved in receptor
 FT binding"
 FT 139..153
 FT /note= "Variable loop region involved in receptor
 FT binding"
 FT 161..164
 FT /note= "Variable loop region involved in receptor
 FT binding"
 FT Domain

KW	Interleukin-1 zeta; IL-1 zeta; splice variant; human; TD2.1.
KW	testis-derived zeta variant; therapy; inflammation; fever.
XX	
OS	Homo sapiens.
XX	
PN	WO200036108-A2.
XX	
PD	22-JUN-2000.
XX	
XX	14-DEC-1999; 99WO-US29549.
XX	
PR	14-DEC-1998; 98US-0112163.
PR	10-NOV-1999; 99US-0164675.
XX	
PA	(IMMUNEX CORP.
XX	
PI	Sims JE, Smith DE, Born TL;
XX	
DR	WPI: 2000-442387/38.
DR	N-PSDB; AAA27920.
XX	
PT	Isolated interleukin-1 (IL-1) zeta nucleic acids and splice variants
PT	TD2.1, TD2.2, TD3 and their encoding proteins, useful as probes for
PT	identifying genes associated with diseases such as glaucoma, and
PT	insulin-dependent diabetes mellitus -
XX	
PS	Claim 10; Page 11; 87pp; English.
XX	
CC	The present sequence is that of splice variant TD2.1 (testis-derived
CC	zeta variant) of human interleukin-1 zeta (IL-1 zeta). TD2.1 mRNA
CC	is generated from exons 1, 2, 4, 5 and 6 of the IL-1 zeta locus, and
CC	the encoded protein is probably a functional IL-1 like molecule.
CC	TD2.1 mRNA is expressed most strongly in the kidney, skeletal
CC	muscle, testis, prostate, ovary, colon, small intestine, liver,
CC	placenta, lung, tonsil, foetal liver, lymph node and bone marrow.
CC	The invention is directed to novel, purified and isolated IL-1
CC	zeta, its splice variants and Xrec2 polypeptides (see AAY95297-301),
CC	the nucleic acids (see AAA27918-22) encoding such polypeptides,
CC	processes for production of recombinant forms of such polypeptides,
CC	and their uses. The polypeptides can be used to study cellular
CC	processes such as immune regulation, cell proliferation, cell
CC	death, cell migration, cell-to-cell interaction and inflammatory
CC	responses, to identify proteins associated with IL-1 zeta, to
CC	screen for potential inhibitors, and to prepare antibodies. In
CC	particular, they can be used to activate and/or inhibit the
CC	activation of vascular endothelial cells and lymphocytes, induce
CC	and/or inhibit the induction of local tissue destruction and fever,
CC	inhibit and/or stimulate macrophages and vascular endothelial cells
CC	to produce IL-6, induce and/or inhibit the induction of
CC	prostaglandins, nitric oxide synthetase, and metalloproteinases, and
CC	upregulate and/or inhibit the upregulation of molecules on the
CC	surface of vascular endothelial cells.
XX	
XX	
SO	Sequence 218 AA:
XX	
Query Match	88.0%; Score 895; DB 21; Length 218;
Best Local Similarity	100.0%; Pred. No. 1,5e-96;
Matches 169; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	24 PKYVNLNPKKFSIHDDHVKVLYLDGSLNLAIVADKKYIRPEIFPALASSLSASAKGSP1 83
Db	50 PKYKNNLPKFFSIHDDHVKVLYLDGSLNLAIVADKKYIRPEIFPALASSLSASAKGSP1 109
OY	84 LLGVSKEGFCLYCDKDKGSHPSLQJLKKREKIMKLAOKESARRPFIFFRQVGSWMNLES 143
Db	110 LLGVSKEGFCLYCDKDKGSHPSLQJLKKREKIMKLAOKESARRPFIFFRQVGSWMNLES 169
OY	144 AARHGWFICTSCNCPNPVGVTDKFNKRKHIEFSPQVCAKMSSEVSD 192
Db	170 AARHGWFICTSCNCPNPVGVTDKFNKRKHIEFSPQVCAKMSSEVSD 218

AAV91885	standard; protein; 218 AA.
AAV91885	
19-JUL-2000	(first entry)
Primate interleukin-1 like molecule (IL-1-zeta) alternative sequence.	
Primate; interleukin-1 like; IL-1-zeta; systemic inflammation; fever;	
hypoglycemia; plasma iron; plasma zinc; acute liver response;	
plasma copper.	
Mammalia.	
Key	Location/Qualifiers
Domain	58..64
Domain	/label= beta_strand_1
Domain	69..74
Domain	/label= beta_strand_2
Domain	76..80
Domain	/label= beta_strand_3
Domain	91..96
Domain	/label= beta_strand_4
Binding-site	100..106
/note= "forms a loop which is part of a primary binding	
segment to the IL-1 receptor type"	
Domain	107..113
Domain	/label= beta_strand_5
Domain	118..126
Domain	/label= beta_strand_6
Domain	131..136
Domain	/label= beta_strand_7
Domain	154..161
Domain	/label= beta_strand_8
Domain	163..169
Domain	/label= beta_strand_9
Domain	176..180
Domain	/label= beta_strand_10
Domain	185..204
Domain	/label= beta_strand_11
Domain	201..204
Domain	/label= beta_strand_12
WO200017363-A2.	
30-MAR-2000.	
17-SEP-1999;	99NO-US20868.
18-SEP-1998;	98US-0156966.
(SCHE) SCHERING CORP.	
Timans JC;	
WPI: 2000-283588/24.	
N-PSDB; AAA08513.	
New mammalian interleukin 1 like molecule, designated IL-1-zeta, useful	
for diagnostic and therapeutic purposes, comprises a 128 amino acid	
sequence	
Claim 1; Page 103-104; 110pp; English.	
The present sequence is an alternative primate interleukin-1 like	
molecule, designated IL-1-zeta. The 12 beta strands, indicated in the	
features table, fold into a beta-trefoil fold. The specification claim	
an isolated or recombinant polypeptide that: (a) specifically binds	
polyclonal antibodies generated against at least a 12 consecutive amino	
acid segment of IL-1-zeta (see AAV91884) or its allelic variant (see	
AAV91885); and (b) comprises at least one sequence selected from:	
AAV91886-903 or AAV91904-06. The preferred 12 consecutive amino acid	

	CC	segment is chosen from AAY91907-18 or AAY91919-21. IL-1-zeta is likely
	CC	to play a role in systemic inflammatory reactions, such as fever, the
	CC	hypoglycemia, reduced plasma iron and zinc, the acute response of the
	CC	liver, and increase plasma copper. IL-1-zeta binding compounds
	CC	(comprising antigen binding sites) and IL-1-zeta polypeptides are also
	CC	useful for both diagnostic and therapeutic purposes.
	XX	
SO	Sequence	218 AA:
	Query Match	88.0%; Score 895; DB 21; Length 218;
	Best Local Similarity	100.0%; Pred. No. 1.5e-96;
	Matches	169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	24	PKVKLNFKKRSIHDDHKVLYLDSGNLIAYPDKNYIRPEIFPALASSLSASAKGSP I 83
DB	50	PKVKLNFKKFSIHDDHKVLVLDSGNLIAYPDKNYIRPEIIFALASSLSASAKGSP I 109
OY	84	ILGVSKGEFCYLCDKDQSHPSLDLKKKEKMLAAOKESARRPIIFYRAOVGSNNMES 143
DB	110	ILGVSKGEFCYLCDKDQSHPSLDLKKKEKMLAAOKESARRPIIFYRAOVGSNNMLES 169
OY	144	AAHPGFICTSCNCPNPVGVTDKPFENRKHIEFSGPVCASEKSPSEVS D 192
DB	170	AAHPGFICTSCNCPNPVGVTDKPFENRKHIEFSGPVCASEKSPSEVS D 218
	RESULT 11	
	AAG68116	
ID	AAG68116 standard; Protein; 218 AA.	
XX	AAG68116;	
XX	22-JAN-2002 (first entry)	
DT		
XX	Human interleukin 1 family protein SPQ ID NO:2.	
DE		
XX	Human; interleukin 1; IL-1; growth factor; Tango-77; diagnosis;	
KW	Identification.	
XX		
OS	Homo sapiens.	
XX		
PN	JP2001231578-A.	
XX		
PD	28-AUG-2001.	
XX		
XX	07-DEC-2000; 2000JP-0372864.	
PF		
XX	09-DEC-1999; 99JP-0349780.	
PR		
XX		
PA	(KYOW) KYOMA HAKKO KOGYO KK.	
XX		
DR	WPI: 2001-609968/70.	
XX	N-PsDB; AAI71179.	
PT	An IL-1 family protein, used for the development of diagnostic and	
PT	treatment agents -	
PS	Claim 1; Page 30; 38pp; Japanese.	
XX		
CC	The present sequence represents a human interleukin 1 (IL-1) family	
CC	protein having a combining affinity to a receptor of a protein of	
CC	human IL-1 family higher than Tango-77. The protein is useful for the	
CC	development of diagnostic, treating and/or preventive agents for	
CC	various diseases.	
XX		
SO	Sequence	218 AA:
	Query Match	88.0%; Score 895; DB 22; Length 218;
	Best Local Similarity	100.0%; Pred. No. 1.5e-96;
	Matches	169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	24	PKVKLNFKKRSIHDDHKVLYLDSGNLIAYPDKNYIRPEIIFALASSLSASAKGSP I 83

```
Db 50 PKVKNLNPKKFSIHDDHKVLYLDGSLNLAVPDKNTIREPIFFALASSLSASAEKGSPI 109
QY 84 LLGYSKGEFCLYCDKDGSHPSLOLKKELMKLAQKESARRPFIIFYRAQVGSNNMLES 143
Db 110 LLGYSKGEFCLYCDKDGSHPSLOLKKELMKLAQKESARRPFIIFYRAQVGSNNMLES 169
QY 144 AAHGWFICTSCNCPNEPVGTDKFENRKHIEFSFQVCAKEMSPSEVSD 192
Db 170 AAHGWFICTSCNCPNEPVGTDKFENRKHIEFSFQVCAKEMSPSEVSD 218

RESULT 12
AAB85136
ID AAB85136 standard; Protein; 218 AA.
AC AAB85136;
XX
XX 22-AUG-2001 (first entry)
XX
XX Interleukin-1 homologue (IL-1H4) polypeptide.
XX
XX Interleukin-1; IL-1H4; antiinflammatory; antibacterial; antiallergic;
XX immunosuppressive; antiporiatic; antiarthritic; cytostatic; antiHIV;
XX cerebroprotective; antiasthmatic; vasotropic; vulnerrary; osteopathic;
XX immunostimulant; antiarteriosclerotic; nootropic; neuroprotective;
XX gene therapy; vaccine.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..20
XX /note="signal peptide"
XX Cleavage-site 20..21
XX Protein 21..218
XX /note="specifically claimed mature protein (AAB85138)"
XX
XX W0200140247-A1.
XX
XX 07-JUN-2001.
XX
XX 30-NOV-2000; 2000MO-US32521.
XX
XX 01-DEC-1999; 99US-0452140.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX Kumar S, McDonnell PC, Young PR;
XX
XX WPI: 2001-389949/41.
XX N-PSDB; AAF84120.
XX
XX Novel interleukin-1 homologue, IL-1H4, for treating chronic and acute
XX inflammation, septicemia, autoimmune diseases, transplant rejection,
XX graft versus host disease, stroke, ischemia, allergy and asthma
XX
XX Examples; Page 29; 30pp; English.
XX
XX The invention provides an isolated interleukin-1 homologue, IL-1H4
XX polypeptide. The IL-1H4 polypeptide can be expressed by standard
XX recombinant methodology. The IL-1H4 polypeptide, polynucleotides and
XX modulators are useful for treating chronic and acute inflammation,
XX septicemia, autoimmune diseases (e.g., inflammatory bowel disease,
XX psoriasis and arthritis), transplant rejection, graft versus host
XX disease, infection, stroke, ischemia, acute respiratory disease syndrome,
XX allergies, asthma, restenosis, brain injury, AIDS, bone diseases (e.g.,
XX osteoporosis), cancer (e.g., lymphoproliferative disorders), congestive
XX heart failure, atherosclerosis and Alzheimer's disease. The IL-1H4
XX polynucleotides are useful as diagnostic reagents and for chromosome
XX identification. The present sequence represents the IL-1H4 polypeptide.
XX
XX Sequence 218 AA:
XX
Query Match 88.0%; Score 895; DB 22; Length 218;
```

```
Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 24 PKVKNLNPKKFSIHDDHKVLYLDGSLNLAVPDKNTIREPIFFALASSLSASAEKGSPI 83
Db 50 PKVKNLNPKKFSIHDDHKVLYLDGSLNLAVPDKNTIREPIFFALASSLSASAEKGSPI 109
QY 84 LLGYSKGEFCLYCDKDGSHPSLOLKKELMKLAQKESARRPFIIFYRAQVGSNNMLES 143
Db 110 LLGYSKGEFCLYCDKDGSHPSLOLKKELMKLAQKESARRPFIIFYRAQVGSNNMLES 169
QY 144 AAHGWFICTSCNCPNEPVGTDKFENRKHIEFSFQVCAKEMSPSEVSD 192
Db 170 AAHGWFICTSCNCPNEPVGTDKFENRKHIEFSFQVCAKEMSPSEVSD 218

RESULT 13
AAB47186
ID AAB47186 standard; Protein; 218 AA.
AC AAB47186;
XX
XX 29-JUN-2001 (first entry)
XX
XX IL-1 related polypeptide.
XX
XX Interleukin-1-related polypeptide; Hsp-MLT cell; T-cell; inhibition;
XX natural killer activity; immune system; gene therapy;
XX immunodeficiency.
XX
XX Homo sapiens.
XX
XX EP1092773-A2.
XX
XX 18-APR-2001.
XX
XX 11-OCT-2000; 2000EP-0308948.
XX
XX 15-OCT-1999; 99JP-0294493.
XX
XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
XX
XX Ushio S, Nukada Y, Yamamoto K, Kurimoto M;
XX
XX WPI: 2001-275206/29.
XX N-PSDB; AAC85880.
XX
XX New human interleukin-1-related polypeptide and polynucleotide, useful
XX for gene therapy and in developing drugs as regulators of natural
XX killer activity, are capable of inhibiting natural killer activity
XX
XX Claim 1; Page 12; 15pp; English.
XX
XX This sequence represents an interleukin-1 (IL-1)-related polypeptide.
XX IL-1 related polypeptide was isolated from Hsp-MLT cells, FERM-BP-2430,
XX an established human T-cell line. IL-1 related polypeptide is useful
XX for inhibiting natural killer (NK) activity, which is related to the
XX immune system of mammals. The DNA encoding the IL-1 related polypeptide
XX is useful in gene therapy of patients in need of NK activity inhibition
XX and others suffering from immunodeficiency.
XX
XX Sequence 218 AA:
XX
Query Match 88.0%; Score 895; DB 22; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 24 PKVKNLNPKKFSIHDDHKVLYLDGSLNLAVPDKNTIREPIFFALASSLSASAEKGSPI 83
Db 50 PKVKNLNPKKFSIHDDHKVLYLDGSLNLAVPDKNTIREPIFFALASSLSASAEKGSPI 109
QY 84 LLGYSKGEFCLYCDKDGSHPSLOLKKELMKLAQKESARRPFIIFYRAQVGSNNMLES 143
```

Db 110 LIGVSKGEFCLYCDKDGQSHPSLQJLKKELMKLAQKESARRPFIYRAQVGSNMLES 169
OY 144 AAHPGWFICTSCNCPNPGVTDKFNKRKHIEFSPVCAKMSPEVSD 192
170 AAHPGWFICTSCNCPNPGVTDKFNKRKHIEFSPVCAKMSPEVSD 218

RESULT 14

AA71084
ID AA71084 standard; Protein; 218 AA.

XX AC AA71084;

XX DT 05-SEP-2000 (first entry)

XX DE Human zilla4-E200D variant protein.

XX XX Human interleukin-1; IL-1; zilla4 protein; inflammation; arthritis;
KW psoriasis; septic shock; graft-versus-host disease; leukaemia; cancer;
KW anaemia; inflammatory bowel disease; acute neuropathology; shock;
KW chronic neuropathology; respiratory disease syndrome; restenosis;
KW acquired immune deficiency syndrome; AIDS; antiinflammatory; cytostatic;
KW anti-arthritis; anti-psoriatic; antibacterial; immunosuppressive;
KW anti-anaemic; neuroprotective; vasotropic; variant;
KW anti-human immunodeficiency virus; HIV.

XX OS Homo sapiens.

XX PN WO200024899-A2.

XX PD 04-MAY-2000.

XX PE 27-OCT-1999; 99WO-US25038.

XX PR 27-OCT-1998; 98US-0179614.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI West RR, Sheppard PO, Gao Z;

XX DR WPI: 2000-350740/30.

XX PT Immunomodulatory interleukin-1 homolog zilla4 proteins, useful for
XX treatment of e.g. arthritis, psoriasis, septic shock, graft-versus-host
XX disease, leukemia -

XX PS Claim 3; Page -: 88pp; English.

XX XX The present sequence is a variant of human interleukin (IL)-1
CC homolog zilla4 protein, consisting of Glu (200) with Asp results in
CC position 200. The replacement of Asp (200) with Asp results in
CC attenuation of pro-inflammatory activity of zilla4 protein.
CC The zilla4 proteins modulate inflammation and other
CC immunological processes and are therefore useful for treatment of
CC arthritis, psoriasis, septic shock, graft-versus-host disease and
CC leukaemia. Other diseases that may be modulated by zilla4 proteins
CC include cancer, anaemia, inflammatory bowel disease, acute and chronic
CC neuropathologies, shock, respiratory disease syndrome, restenosis and
CC acquired immune deficiency syndrome.
CC Note: The present sequence is not shown in the specification but is
CC derived from human zilla4 protein sequence shown in figure-2 (AA70927).

XX SQ Sequence 218 AA;

Query Match 87.7%; Score 892; DB 21; Length 218;
Best Local Similarity 99.4%; Pred. No. 3.3e-96;
Matches 168; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 24 PKVKMLNPKKFSIHDDKVLVDSGNLIAPDKNYIRPEIFPALASSLSASAEKGSPI 83
DB 50 PKVKMLNPKKFSIHDDKVLVDSGNLIAPDKNYIRPEIFPALASSLSASAEKGSPI 109
OY 84 LIGVSKGEFCLYCDKDGQSHPSLQJLKKELMKLAQKESARRPFIYRAQVGSNMLES 143

Db 110 LIGVSKGEFCLYCDKDGQSHPSLQJLKKELMKLAQKESARRPFIYRAQVGSNMLES 169
OY 144 AAHPGWFICTSCNCPNPGVTDKFNKRKHIEFSPVCAKMSPEVSD 192
170 AAHPGWFICTSCNCPNPGVTDKFNKRKHIEFSPVCAKMSPEVSD 218

RESULT 15

AA70933
ID AA70933 standard; Protein; 218 AA.

XX AC AA70933;

XX DT 05-SEP-2000 (first entry)

XX DE Human zilla4-E200K variant protein.

XX XX Human interleukin-1; IL-1; zilla4 protein; inflammation; arthritis;
KW psoriasis; septic shock; graft-versus-host disease; leukaemia; cancer;
KW anaemia; inflammatory bowel disease; acute neuropathology; shock;
KW chronic neuropathology; respiratory disease syndrome; restenosis;
KW acquired immune deficiency syndrome; AIDS; antiinflammatory; cytostatic;
KW anti-arthritis; anti-psoriatic; antibacterial; immunosuppressive;
KW anti-anaemic; neuroprotective; vasotropic;
KW anti-human immunodeficiency virus; HIV.

XX OS Homo sapiens.

XX PN WO200024899-A2.

XX PD 04-MAY-2000.

XX PE 27-OCT-1999; 99WO-US25038.

XX PR 27-OCT-1998; 98US-0179614.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI West RR, Sheppard PO, Gao Z;

XX DR WPI: 2000-350740/30.
XX DR N-PSDB; AAD00212.

XX PT Immunomodulatory interleukin-1 homolog zilla4 proteins, useful for
XX treatment of e.g. arthritis, psoriasis, septic shock, graft-versus-host
XX disease, leukemia -

XX PS Claim 8; Page 77-78; 88pp; English.

XX XX The present sequence is a variant of human interleukin (IL)-1
CC homolog zilla4 protein designated zilla4-E200K. The replacement of
CC Glu (200) with Lys results in change in activity from agonist to
CC antagonist. The zilla4 proteins modulate inflammation and other
CC immunological processes and are therefore useful for treatment of
CC arthritis, psoriasis, septic shock, graft-versus-host disease and
CC leukaemia. Other diseases that may be modulated by zilla4 proteins
CC include cancer, anaemia, inflammatory bowel disease, acute and chronic
CC neuropathologies, shock, respiratory disease syndrome, restenosis and
CC acquired immune deficiency syndrome.

XX SQ Sequence 218 AA;

Query Match 87.6%; Score 891; DB 21; Length 218;
Best Local Similarity 99.4%; Pred. No. 4.3e-96;
Matches 168; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 24 PKVKMLNPKKFSIHDDKVLVDSGNLIAPDKNYIRPEIFPALASSLSASAEKGSPI 83
DB 50 PKVKMLNPKKFSIHDDKVLVDSGNLIAPDKNYIRPEIFPALASSLSASAEKGSPI 109
OY 84 LIGVSKGEFCLYCDKDGQSHPSLQJLKKELMKLAQKESARRPFIYRAQVGSNMLES 143

Db 110 LIGVSKGEFCLYCDKDKGSHPSLOLKKKELMKLIAAQKESARRPFIYRAQVGSWMLES 169
OY 144 AAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSFOPVCKAKEMSPSEVSD 192
|||
Db 170 AAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSFOPVCKAKEMSPSEVSD 218
|||

Search completed: May 3, 2003, 18:34:24
Job time : 94 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2003, 18:30:35 ; Search time 73 Seconds
(without alignments)
252.847 Million cell updates/sec

Title: US-09-876-790-3

Perfect score: 1017
Sequence: 1 MSGCDRETEETKGNKSPFKR.....IEFSPOVCKAEMSPSEVSD 192

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR-73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	172.5	17.0	155	JC7104	interleukin-1 rece
2	159	15.6	178	A44610	interleukin-1 rece
3	151.5	14.9	177	A54377	interleukin-1 rece
4	150.5	14.8	180	A39386	interleukin-1 rece
5	149.5	14.7	177	A30368	interleukin-1 rece
6	144.5	14.2	178	C40956	interleukin-1 rece
7	127.5	12.5	266	S23010	interleukin-1 beta
8	119.5	11.8	267	JN0724	interleukin-1 beta
9	112.5	11.1	266	ICB01B	interleukin-1 beta
10	112.5	11.1	267	S38373	interleukin-1 beta
11	104	10.2	269	I55969	interleukin-1 beta
12	93	9.1	269	ICB01B	interleukin-1 beta
13	91	8.9	404	S34031	KTR3 protein - yea
14	89.5	8.8	214	UC5646	interleukin-1 beta
15	89	8.8	268	A30584	interleukin-1 beta
16	84	8.3	270	ICM61	interleukin-1 alpha
17	81	8.0	776	S67053	probable membrane
18	80.5	7.9	571	D86164	hypothetical prote
19	80.5	7.9	845	T17291	hypothetical prote
20	80.5	7.9	3190	T13828	CREB-binding prote
21	79.5	7.8	1199	T15826	hypothetical prote
22	79	7.6	859	C87358	hypothetical prote
23	76.5	7.5	627	T02846	dynamin light chain
24	76	7.5	425	T24522	hypothetical prote
25	76	7.5	448	JN0118	glucan 1,3-beta-gl
26	76	7.5	914	B96592	hypothetical prote
27	75	7.4	361	S23346	hypothetical prote
28	74.5	7.3	256	S37926	hypothetical prote
29	74.5	7.3	1151	T04657	hypothetical prote

30	74	7.3	545	2	T19172	hypothetical prote
31	74	7.3	803	2	E81804	hypothetical prote
32	74	7.3	1116	2	T14598	polyprotein - slim
33	73.5	7.2	460	2	T47709	glucuronosyl trans
34	73	7.2	201	2	E81309	nitroreductase Cjl
35	73	7.2	231	2	S59589	histone H1 - Chlam
36	73	7.2	317	2	AH0351	hypothetical prote
37	73	7.2	453	2	C90568	hypothetical prote
38	72.5	7.1	247	2	T50286	hypothetical prote
39	72.5	7.1	351	2	T19372	hypothetical prote
40	72.5	7.1	685	2	E82297	c-di-GMP phosphodi
41	72.5	7.1	933	2	G70166	probable zinc prot
42	72	7.1	307	2	E86323	protein F14D16.11
43	72	7.1	1034	2	B86880	SMI/SNF family hel
44	71.5	7.0	224	2	D90213	conserved hypotbet
45	71.5	7.0	268	1	A61246	interleukin-1 alpha

ALIGNMENTS

```
RESULT 1
JC7104
interleukin-1 receptor antagonist - human
C:Species: Homo sapiens (man)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C:Accession: JC7104
R:Mulero, J.J.; Pace, A.M.; Neiken, S.T.; Loeb, D.B.; Correa, T.R.; Drmanac, R.; For
Biochem. Biophys. Res. Commun. 263, 702-706, 1999
A:Title: IL1AHL1: A novel interleukin-1 receptor antagonist gene.
A:Reference number: JC7104; MUID:99443727; PMID:10512743
A:Accession: JC7104
A:Molecule type: mRNA
A:Residues: 1-155 <MUI>
A:Cross-References: GB:AF186094; NID:96049804; PIDN:AAF02757.1; PID:96049805
C:Genetics:
A:Gene: il1hl1
A:Map position: 2q14
C:Keywords: macrophage

Query Match          17.0%; Score 172.5; DB 2; Length 155;
Best Local Similarity 33.6%; Pred. No. 4.2e-09;
Matches 51; Conservative 17; Mismatches 47; Indels 37; Gaps 6;

QY 34 FSIHDDHKVYLVDGSLNLAIVDPKNTIRPEIFALASSLSASAEK----- 80
DB 9 FRKKDALKVLYLHNQL-----LAGGLAGKVIKGEISVPPNRWIDA 52
QY 81 --SPILGVSKGEFCYCDKDGQSHPSLQKKELMKL-AAOKESARPPFIYPAOYGS 137
DB 53 SLSPVLGVQGGSGCISC--GWGO-EPTLTLEPVNIMELYLAKES--KSFTFYRDGKL 107
QY 138 WNNLESAAHPGFICTSCNCPNEPVGVTDKFEEN 169
DB 108 TTSFESAAYGWPICVTVPADQPVRLTQLPEN 139

RESULT 2
A44610
interleukin-1 receptor antagonist precursor - mouse
N:Alternate names: IL-1RA
C:Species: Mus musculus (house mouse)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 16-Jul-1999
C:Accession: A44610; B40956; A49031; T56106; I52970
R:Matsumura, H.; Rousset, M.F.; Matsushima, K.; Hishinuma, A.; Sherr, C.J.
Blood 78, 616-623, 1991
A:Title: Cloning and expression of murine interleukin-1 receptor antagonist in macroph
A:Reference number: A44610; MUID:91316273; PMID:1830498
A:Accession: A44610
A:Molecule type: mRNA
A:Residues: 1-178 <MUI>
A:Cross-References: GB:M64404; NID:9198296; PIDN:AAA39277.1; PID:9198297
R:Eisenberg, S.F.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thomp-
```

Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991

A>Title: Interleukin 1 receptor antagonist is a member of the interleukin-1 gene family

A:Reference number: A40956; MUID:91271363; PMID:182886

A:Accession: R40956

A:Molecule type: DNA

A:Residues: 7-178 <EIS>

A:CROSS-references: GB:M63100; NID:g198389; PIDN:AAA9310.1; PID:g198390

R.Shuck, M.E.; Eessalu, T.E.; Tracey, D.E.; Bienkowski, M.J.

Eur. J. Immunol. 21, 2775-2780, 1991

A>Title: Cloning, heterologous expression and characterization of murine Interleukin 1

A:Reference number: A49031; MUID:92037824; PMID:1834470

A:Accession: A49031

A:Molecule type: mRNA

A:Residues: 23-178 <SHU>

A:CROSS-references: GB:S64082; NID:g238584; PIDN:AAB20265.1; PID:g238585

A:Experimental source: peritoneal macrophages, ICR strain

A>Note: sequence extracted from NCBI backbone (NCBIT:64082, NCBI:P:64085)

R.Zahedi, K.; Seldin, M.F.; Rife, M.; Ezekowitz, R.B.; Whitehead, A.S.

J. Immunol. 146, 4228-4233, 1991

A>Title: Mouse IL-1 receptor antagonist protein: Molecular characterization, gene map

A:Reference number: 156106; MUID:91250712; PMID:1828262

A:Accession: 156106

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-178 <RES>

A:CROSS-references: GB:M74294; NID:g198387; PIDN:AAA39309.1; PID:g198388

R.Zahedi, K.A.; Unlur, C.M.; Rife, M.; Prada, A.E.; Whitehead, A.S.

Cytokine 6, 1-9, 1994

A>Title: The mouse interleukin 1 receptor antagonist protein: gene structure and regula

A:Reference number: 152970; MUID:94271931; PMID:8003626

A:Accession: 152970

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-178 <RE2>

A:CROSS-references: GB:L32838; NID:g487864; PIDN:AAA20576.1; PID:g528978

A:Genetics:

A:Gene: IL-1rn

A:introns: 40/2; 70/1; 107/3

C:Superfamily: Interleukin-1

C:Keywords: cytokine receptor

F:1.26/Domain: signal sequence #status predicted <SIG>

F:2.17/Product: Interleukin-1 receptor antagonist #status predicted <MA2>

Query Match 15.6%; Score 159; DB 2; Length 178;
Best Local Similarity 32.7%; Pred. No. 9, 6e-08;
Matches 48; Conservative 23; Mismatches 64; Indels 12; Gaps 7;

OY 34 FSIHQDHKVLVLDGNIIVDPKNYIR-PEIFALASSLSASAEGSPILLGVSGEF 92
| | | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 39 FRIMPTNQKTFLRNNOILIA---GYLOGPNI--KLEIKIMVPIDLHS-VFLGIHGKL 91
| | | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 93 CLYCQDKXGQSHPSIQLKKEKLMKLAOKESARRRPIRYAQQVSMMNLSEAHPGWIC 152
| | | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 92 CLSCAKSDDI-KQLLEEVNITDLSKKNEEDKR-FTFIREKGPTTSFEESAACPGWPLC 148
| | | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 153 TSCNCEPVGYTDKFENRKHI-EFSFQ 178
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 149 TTLADRPVSLNTMPDEPLYVTKEFFQ 175
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 3
A54377
Interleukin-1 receptor antagonist secreted form precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C:Accession: A54377; I46729
R:Cominelli, F.; Borjolami, M.; Pizarro, T.T.; Monsacchi, L.; Ferretti, M.; Brewer, M.T.
J. Biol. Chem. 269, 6962-6971, 1994
A>Title: Rabbit Interleukin-1 receptor antagonist. Cloning, expression, functional charact

A:Reference number: A54377; MUID:94165101; PMID:7509813

A:Accession: A54377

A:Molecule type: mRNA

A:Residues: 1-177 <COM>

```

A:Cross-references: GB:S68977; NID:g545740; PIDN:AAB30093.1; PID:g545741
A:Experimental source: colon tissue
A>Note: Sequence extracted from NCBI backbone (NCBIN:144168, NCBIP:144169)
R:Goto, F.; Goto, K.; Miyata, T.; Ohkawara, S.; Takao, T.; Mori, S.; Furukawa, S.; Ma
Immunology 77, 235-244, 1992
A>Title: Interleukin-1 receptor antagonist in inflammatory exudate cells of rabbits. P
A:Reference number: I46729; MUID:93052512; PMID:1427977
A:Accession: I46729
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-177 <GDS>
A:Cross-references: GB:D18332; NID:g425767; PIDN:BAA04860.1; PID:g452205
C:Superfamily: interleukin-1
C:Keywords: cytokine receptor; extracellular protein; glycoprotein
F:1-25/Domain: signal sequence #status predicted <Sig>
F:109/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          14.9%; Score 151.5; DB 2; Length 177;
Best Local Similarity 26.9%; Pred. No. 5e-07;
Matches 47; Conservative 25; Mismatches 50; Indels 53; Gaps 7;

Oy 9 TETGRKNSFKRRKRGPKVKNLNPKKFSIHDDHKVLVDSCNLIA----- 53
    :: : : : : : : : : : : : : : : : : : : : : : : : : :
Db 21 SETACRPQSGKRRCR-----MQAFRIWDVNQKTFFLRNNQLVAGYLGPNNALERID 72
    :: : : : : : : : : : : : : : : : : : : : : : : : : :

Oy 54 -VPDKNYIRPELFPLASLSASAENKGSPIILGVSKKEFLYCDK--DKQSHPISLDK 110
    || : : : : : : : : : : : : : : : : : : : : : : : : :
Db 73 VVP-----LEPOLF-----LGIQRKGLCLSCVSKSDKKMLH----LE 106
    || : : : : : : : : : : : : : : : : : : : : : : : : :

Oy 111 KEKLKLAOKESARPFIFRYAGVSWMNLESAAHPMFICTGCNCEPAGVTD 165
    :: : : : : : : : : : : : : : : : : : : : : : : : : :
Db 107 AVNIITDLCKNKNEQDKR-FTFIRSNGPTTTESSACPEMFICTALADQPVSLTIN 160
    || : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 4
A39386
Interleukin-1 receptor antagonist, long intracellular splice form - human
NtContains: interleukin-1 receptor antagonist, short intracellular splice form
C:Species: Homo sapiens (man)
C:Date: 28-Feb-1992 #sequence-revision 11-Apr-1997 #text-change 26-May-2000
C:Accession: J37893; A39386
R:Muñoz, M.; Polentarutti, N.; Sironi, M.; Poli, G.; De Girola, L.; Introna, M.; Mantov
J. Exp. Med. 182, 623-628, 1995
A>Title: Cloning and characterization of a new isoform of the interleukin 1 receptor
A:Reference number: I37893; MUID:9535865; PMID:7629520
A:Accession: J37893
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-180 <RES>
A:Cross-references: EMBL:X84348; NID:g1008970; PIDN:CAA59087.1; PID:g1008971
R:Haskill, S.; Martin, G.; Van Le, L.; Morris, J.; Pearce, A.; Biglier, C.F.; Jaffe, G.
Proc. Natl. Acad. Sci. U.S.A. 88, 3681-3685, 1991
A>Title: cDNA cloning of an intracellular form of the human interleukin 1 receptor an
A:Reference number: A39386; MUID:91219436; PMID:1827201
A:Accession: A39386
A:Molecule type: mRNA
A:Residues: 1-3,25-180 <HAS>
A:Cross-references: GB:M55646; NID:g186291; PIDN:AAA59138.1; PID:g186292
C:Comment: For an alternative splice form, see PIR:A30368
C:Genetics:
A:Gene: GDB:IL1RN
A:Cross-references: GDB:I25897; OMIM:147679
A:Map position: 2q14.2-q14.2
C:Superfamily: interleukin-1
C:Keywords: alternative splicing; cytokine receptor
F:1-180/Product: interleukin-1 receptor antagonist, long intracellular splice form #s
F:1-3,25-180/Product: interleukin-1 receptor antagonist, short intracellular splice f

Query Match          14.8%; Score 150.5; DB 2; Length 180;
Best Local Similarity 28.0%; Pred. No. 6.3e-07;
Matches 46; Conservative 29; Mismatches 64; Indels 25; Gaps 8;

```



```

Db      22 DSKETICPSGRKSSKM-----CAFRIMVYNQKTFYLRNNQLVA-----GYLG 65
Oy      62 PEIFPALASSLSASAEKSPILLGVSKGEFLCYCDKKGQSHPSIQLKKEKIMLAQK 121
      66 PNV--NLEEKIDVPIEPHA-LFLGHGKMCCLSCVKSDEFR--LQLEAVNITDLSENR 120
Oy      122 ESARRPFIFRYAOGVSWNMLESAAHPGWFICTSCNCEPVGATD 165
      121 KQDKR-FAFIRSDSGPTTSFESAACPGWFICTMEADQPVSLTN 163

RESULT 5
Interleukin-1 receptor antagonist secreted form precursor - human
C:Species: Homo sapiens (man)
C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 26-May-2000
C:Accession: A40956; I37894; A30368; S08160; S08159; A37822
R:Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson,
Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A>Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family:
A:Reference number: A40956; MUID:91271363; PMID:1828896
A:Accession: A40956
A:Molecule type: DNA
A:Residues: 1-177 <EIS>
R:Lennard, A.; Gorman, P.; Carrier, M.; Griffiths, S.; Scootney, H.; Sheer, D.; Solari, R
Cytokine 4, 83-89, 1992
A>Title: Cloning and chromosome mapping of the human interleukin-1 receptor antagonist g
A:Reference number: I37894; MUID:92338323; PMID:1385987
A:Accession: I37894
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-177 <LEN>
A:Cross-references: EMBL:X64532; NID:g33798; PIDN:CAA45832.1; PID:g33799
R:Cartier, D.B.; Delbel Jr., M.R.; Dunn, C.J.; Tomich, C.S.C.; Laborde, A.L.; Slightom, J
J.G.; Siew, L.C.; Hardee, M.M.; Zurcher-Neely, H.A.; Reardon, I.M.; Heinrikson, R.L.; Tr
Nature 344, 633-638, 1990
A>Title: Purification, cloning, expression and biological characterization of an interle
A:Reference number: A30368; MUID:90220867; PMID:2139180
A:Accession: A30368
A:Molecule type: mRNA
A:Residues: 1-177 <CAR>
A:Cross-references: GB:X53296; NID:g32578; PIDN:CAA37386.1; PID:g32579
R:Ettenberg, S.P.; Evans, R.J.; Arend, W.P.; Verderber, E.; Brewer, M.T.; Hannum, C.H.;
Nature 343, 341-346, 1990
A>Title: Primary structure and functional expression from complementary DNA of a human I
A:Reference number: S08160; MUID:90136921; PMID:2137201
A:Accession: S08160
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-177 <E12>
A:Cross-references: GB:X52015; NID:g32576; PIDN:CAA36262.1; PID:g32577
R:Hannum, C.H.; Wilcox, C.J.; Arend, W.P.; Joslin, F.G.; Drilps, D.J.; Heimdal, P.L.; Ar
Nature 343, 336-340, 1990
A>Title: Interleukin-1 receptor antagonist activity of a human interleukin-1 inhibitor.
A:Reference number: S08159; MUID:90136920; PMID:2137200
A:Accession: S08159
A:Molecule type: protein
A:Residues: 26-75;97-108;110-116;120-131;163-176 <HAN>
R:Blenkowsky, M.J.; Eessalu, T.E.; Berger, A.E.; Truesdell, S.E.; Shelly, J.A.; Laborde,
J. Biol. Chem. 265, 14505-14511, 1990
A>Title: Purification and characterization of interleukin 1 receptor level antagonist pr
A:Reference number: A37822; MUID:90354444; PMID:2143761
A:Accession: A37822
A:Molecule type: protein
A:Residues: 26-52;70-77;122-127;170-175 <BIE>
C:Experimental source: culture medium, PMA-stimulated THP-1 cells
C:Comment: For an alternative splice form, see PIR:A39386
C:Genetics:
A:Gene: GDB:IL1RN
A:Cross-references: GDB:125897; OMIM:147679

```

```

A:Map position: 2q14.2-2q14.2
A:Introns: 39/2; 69/1; 106/3
C:Superfamily: interleukin-1
C:Keywords: alternative splicing; cytokine receptor; extracellular protein; glycopro
F:1-25/Domains: signal sequence #status predicted <Sig>
F:26-177/Product: interleukin-1 receptor antagonist #status experimental <Mat>
F:109/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match      14.7%; Score 149.5; DB 2; Length 177;
Best Local Similarity 29.3%; Pred. No. 7.7e-07;
Matches 41; Conservative 28; Mismatches 60; Indels 11; Gaps 6;

Oy      27 KNINPKFESIHQDHRKVLVDSGNLIAVPDKYIR-PEIFPALASSLSASAEKSPILL 85
      31 KSKKQAFRIWYNQKTFYLRNNQLVA-----GYLGPNV--NLEEKIDVPIEPHA-LFL 83
Oy      86 GVSKEGFLCYCDKKGQSHPSIQLKKEKIMLAQKESARRPFIFRYAOGVSWNMLESAA 145
      84 GIHGKMCCLSCVKSDEFR--LQLEAVNITDLSENRKQDKR-FAFIRSDSGPTTSFESAA 140
Oy      146 HPGWFICTSCNCEPVGATD 165
      141 CPGWFLCTAMEADQPVSLTN 160

RESULT 6
Interleukin-1 receptor antagonist precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 16-Jul-1999
C:Accession: C40956
R:Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thomp
Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A>Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene fam
A:Reference number: A40956; MUID:91271363; PMID:1828896
A:Accession: C40956
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-178 <EIS>
A:Cross-references: GB:M63101; NID:g204928; PIDN:AAA41434.1; PID:g204929
C:Superfamily: Interleukin-1
C:Keywords: cytokine receptor

Query Match      14.2%; Score 144.5; DB 2; Length 178;
Best Local Similarity 29.1%; Pred. No. 2.3e-06;
Matches 41; Conservative 20; Mismatches 53; Indels 27; Gaps 4;

Oy      34 FSIHQDHRKVLVDSGNLIA-----VPDKYIRPEIFPALASSLSASAEKSPILL 84
      39 FRIMPTNQKTFYLRNNQLIAGYLGCPNTRLEEKIDVPIDF-----RNVF 83
Oy      85 LGVSKGEFLCYCDKKGQSHPSIQLKKEKIMLAQKESARRPFIFRYAOGVSWNMLESAA 144
      84 LGIHGKMCCLSCVKSDDT--LQLEAVNITDLSNKKEDKR-FTFIRSETGPTTSFESL 140
Oy      145 AHGWFICTSCNCEPVGATD 165
      141 ACPGWFLCTMEADQPVSLTN 161

RESULT 7
Interleukin-1 beta precursor - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C>Date: 08-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 15-Oct-1999
R:Seow, H.F.; Rothel, J.S.; David, M.J.; Wood, P.R.
DNA Seq. 1, 423-426, 1991
A>Title: Nucleotide sequence of ovine macrophage Interleukin-1 beta cDNA.
A:Reference number: S23010; MUID:92119335; PMID:1840515
A:Accession: S23010
A:Molecule type: mRNA

```

Query Match	12.5%	Score 127.5	DB 1	Length 266
Best Local Similarity	23.5%	Pred. No. 0.00016		
Matches	39	Conservative	26	Mismatches 58; Indels 9; Gaps 6;
QY	33	KFSIHDDQHKVLYLDSG---	NLIAVPDKNYIPETFFALASLSASAEKSGPILLGVSK	89
		↑ : : : : :	: : : : : : : : : : : : : : :	: : : : : : : : : :
Db	120	KCKLQDRGKSLVYLDSPCVLKALHLP	PSQEMSR-EVYFCM-SVYGEERDNKLPVALGIRD	177
QY	90	GEFCLYCDKDKQSGHPSLQLKKEKIM	LAOKESARRPFIIFYRAOVGSMNMLESAHPGM	149
		↑ : : : : : : : : : : : : : : :	: : : : : : : : : : : : : : :	: : : : : : : : : :
Db	178	KNLYLSGCY-KGDT-PIQL-R--E	EVDPKRYPRKRNRKEKRFVFKYETIKNTVEP	SVLYPNW 233
QY	150	FICTSCNCPY	161	
		↑ : : : : : : : : : :		
Db	234	YISTSIQIEKPV	245	

```

C:Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophage; mitogen
F:115-267/Product: Interleukin-1 beta #status predicted <11>
F:77/Binding site: myristate (lys) (covalent) #status predicted

Query Match      11.8%; Score 119.5; DB 1; Length 267;
Best Local Similarity 27.0%; Pred. No. 0.0009;
Matches 37; Conservative 27; Mismatches 64; Indels 9; Gaps 5;

QY 28 NLNKKESIHHQDHKVLVLDSCNLIAPVD--KNYIRPEIFALASSLSASAEGSPILL 85
   | : : : : : | | | | | : : : : : | : : : : : | : : : : : | : :
Db 116 NVQSMCKTLQDKHRSKSLVLAAPHMLKALHLLTGDLKREVCVM-SFVQGDSDNNKIPVTL 174
QY 86 GVSXGEFLYVC-DDDKGQSHPSLQTKKEKLMKLAQKESARPRPIFYRAQVGSNMNMLESA 144
   | : : : : : | : : : : : | : : : : : | : : : : : | : :
Db 175 GIKKGNLYLSVQMKD---NTPFLQL--EDIDPKRYPKDMKRRVFYTKTEIKNRYEFESA 229
QY 145 AHPGWFICTSCNCEPVP 161
Db 230 LYPNMYISTSQAEQKPV 246

RESULT 9
ICB01B
Interleukin-1 beta precursor - bovine
N:Alternate names: hematopoietin-1; IL-1 beta
C:Species: Bos primigenius taurus (cattle)
C>Date: 31-Mar-1989 #sequence, revision 31-Mar-1989 #text, change 22-Jun-1999
C:Accession: J10010; S01380
R:Maliszewski, C.R.; Baker, P.E.; Schoenborn, M.A.; Davis, B.S.; Cosman, D.; Gyllis,
Mol. Immunol. 25, 429-437, 1988
A>Title: Cloning, sequence and expression of bovine interleukin 1-alpha and interleuk
A:Reference number: A94695; MUID:86318652; PMID:3261832
A:Accession: J10010
A:Molecule type: mRNA
A:Residues: 1-266 <MBL>
A:Cross-references: GB:337211; NID:g163200; PIDN:AAA30584.1; PID:g163201
R:Leong, S.R.; Plaggs, G.M.; Iawman, M.; Gray, P.W.
Nucleic Acids Res. 10, 9054, 1988
A>Title: The nucleotide sequence for the cDNA of bovine interleukin-1 beta.
A:Reference number: S01380; MUID:89016591; PMID:3262866
A:Accession: S01380
A:Molecule type: mRNA
A:Residues: 1-251, 'A', 253-266 <LEO>
A:Cross-references: EMBL:X12498; NID:g4448; PIDN:CAA31018.1; PID:g4449
C:Comment: This protein is a cytokine that mediates a variety of immunoregulatory and
C:Comment: This protein lacks a conventional signal sequence for protein export. Clea
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C:Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin
C:Superfamily: Interleukin-1
C:Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F:114-266/Product: Interleukin-1 beta #status predicted <MAT>

Query Match      11.1%; Score 112.5; DB 1; Length 266;
Best Local Similarity 27.5%; Pred. No. 0.0042;
Matches 36; Conservative 25; Mismatches 63; Indels 7; Gaps 5;

QY 33 KFSIHDDHAKVLVLDSCNLIAPVD--KNYIRPEIFALASSLSASAEGSPILLGVSKG 90
   | : : : : : | : : : : : | : : : : : | : : : : : | : :
Db 120 KCKIQQDREQKSLVLAAPCVLKAHLHLLSQEMNREVFQCM-SFVQGEERDNKIPVALGIKDK 178
QY 91 EFLCYCDKDKGQSHPSLQTKKEKLMKLAQKESARPRPIFYRAQVGSNMNIESAHPGWF 150
   | : : : : : | : : : : : | : : : : : | : : : : : | : :
Db 179 NLVYSYCVK-KGDT-PTQLQ--EEVDPRVYVYKRNMKEKRFVFEKTEIKNTVEFESVLYPNWY 234
QY 151 ICTSCNCEPVP 161
Db 235 ISTSQIEERPVP 245

RESULT 10
interleukin-1 beta precursor - pig
C:Species: Sus scrofa domestica (domestic pig)

```


A:Molecule type: mRNA
 A:Residues: 1-269 <NTS>
 A:Cross-references: GB:M15330; NID:9186283; PIDN:AAA59135.1; PID:g307045
 R:Kotenko, S.V.; Bulenkov, M.T.; Velko, V.P.; Epishin, S.M.; Lomakin, I.B.; Emel'yanov, I.I.; Vinetskii, Y.P.
 Dokl. Akad. Nauk SSSR 309, 1005-1008, 1989
 A:Title: Cloning of the cDNA coding for human prointerleukin-1 alpha and prointerleukin-1 beta
 A:Reference number: 138131; MUID:90249285; PMID:2635664
 A:Accession: 138132
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-269 <KOT>
 A:Cross-references: EMBL:X56087; NID:g35662; PIDN:CAA39567.1; PID:g35663
 R:Zsebo, K.M.; Wypych, J.; Vyschenko, V.N.; Lu, H.; Hunt, P.; Dukes, P.P.; Langley, K.; Blood, J.; 962-968, 1988
 A:Title: Effects of hematopoietin-1 and interleukin 1 activities on early hematopoietic A:Reference number: A90732; MUID:88184226; PMID:3281727
 A:Accession: B27616
 A:Molecule type: protein
 A:Residues: 117-123, 'X', 125-126, 'X', 128 <ZSE>
 R:Stevenson, F.T.; Bursien, S.L.; Fenton, C.; Locksley, R.M.; Lovett, D.H. Proc. Natl. Acad. Sci. U.S.A. 90, 7245-7249, 1993
 A:Title: The 31-kDa precursor of interleukin 1alpha is myristoylated on specific lysines A:Reference number: A48293; MUID:93348250; PMID:8346241
 A:Cross-references: EMBL:U00001; NID:9110334; PID:1837236
 R:Manduri, V.B.; Holmes, J.D.; Pan, Y.C.E.; Killian, P.L.; Stern, A.S. Blochm. Biophys. Acta 1118, 25-35, 1991
 A:Title: The role of arginine residues in interleukin 1 receptor binding.
 A:Reference number: S19608; MUID:92110334; PMID:1837236
 A:Contents: annotation: type 1 IL-1 receptor interaction site
 A:Note: modification of Arg-120 by phenylglyoxal blocks receptor binding
 R:Clote, G.M.; Gronenborn, A.M.
 submitted to the Brookhaven Protein Data Bank, January 1991
 A:Reference number: A50049; PDB:611B
 A:Contents: annotation: confirmation by (13)C- and (1)H-NMR, residues 117-269
 R:Clote, G.M.; Wingfield, P.T.; Gronenborn, A.M. Biochemistry 30, 2315-2323, 1991
 A:Title: High-resolution three-dimensional structure of interleukin 1beta in solution by A:Reference number: A44675; MUID:91159409; PMID:2001363
 A:Contents: annotation: (1)H-NMR structural determination
 R:Hazuda, D.J.; Strickler, J.; Simon, P.; Young, P.R. J. Biol. Chem. 266, 7081-7086, 1991
 A:Title: Structure-function mapping of interleukin 1 precursors. Cleavage leads to a core A:Reference number: A39774; MUID:91201363; PMID:2016316
 A:Contents: annotation
 R:Finzel, B.C.; Watenpugh, K.D.; Einspahr, H.M. submitted to the Brookhaven Protein Data Bank, December 1989
 A:Reference number: A50016; PDB:111B
 A:Contents: annotation: X-ray crystallography, 2.0 angstroms, residues 119-269
 J:Finzel, B.C.; Clancy, L.L.; Holland, D.R.; Muchmore, S.W.; Watenpugh, K.D.; Einspahr, J. Mol. Biol. 209, 779-791, 1988
 A:Title: Crystal structure of recombinant human interleukin-1beta at 2.0 angstrom resolution A:Reference number: A44666; MUID:90064532; PMID:2585509
 A:Contents: annotation: X-ray crystallography, 2.0 angstroms
 C:Comment: This protein lacks a conventional signal sequence for protein export. Cleavage of form of interleukin-1beta, unlike interleukin-1-alpha, is inactive.
 C:Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a C:Genetics:
 A:Gene: GDB:IL1B
 A:Cross-references: GDB:120094; OMT:147720
 A:Map position: 2q13-2q21
 A:Introns: 16/2; 33/3; 101/1; 156/1; 199/3
 C:Superfamily: Interleukin-1
 C:Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophage; binding site; myristate (Lys) (covalent) (partial) #status experimental
 F:117-269/Product: Interleukin-1 beta #status experimental <IL1>
 F:123/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 9.1%; Score 93; DB 1; Length 269;
 Best Local Similarity 28.4%; Pred. No. 0.3;
 Matches 40; Conservative 27; Mismatches 58; Indels 16; Gaps 8;

QY 26 VKNLPKPSIHDDHKLVLDSG--NLIAVDKNY-IRPEIFALASSASAKGSP 82

Db 119 VRSLN---CTLRDSQOKSLW-SCPYELKAIHLAQDMEDQVFSNFSFGESNDK-IP 173
 QY 83 ILGVSKGEFCILYC--DKRGQSHPSLQKKKELMLAAQKESARRPFIFRAQVSWNM 140
 Db 174 VALGKKEKNLYLSCVLADDK---PTQL--ESVDPRNRYKKKKKKFVNKLEINNKLE 227
 QY 141 LESAHPEGWFCTSCNCEPEY 161
 Db 228 FESAQFPNMYISTQAEKMPV 248

RESULT 13
 S34031
 KTR3 protein - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein YBR1445; protein YBR205w
 C:Species: Saccharomyces cerevisiae
 C>Date: 30-Sep-1993 #sequence, revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: S34031; S46077; S34928
 R:Jacquet, M.
 submitted to the EMBL Data Library, January 1993
 A:Reference number: S34022
 A:Accession: S34031
 A:Molecule type: DNA
 A:Residues: 1-404 <JAC>
 A:Cross-references: EMBL:Z21487; NID:g311665; PID:g311682
 R:Bussereau, F.; Demolis, N.; Jacquet, M.; Mallet, L. submitted to the Protein Sequence Database, August 1994
 A:Reference number: S46054
 A:Accession: S46077
 A:Molecule type: DNA
 A:Residues: 1-404 <BUS>
 A:Cross-references: EMBL:Z26074; NID:g356582; PID:g356583; MIPS:YBR205w
 R:Bussereau, F.; Mallet, L.; Gallion, L.; Jacquet, M. Yeast 9, 797-806, 1993
 A:Title: Yeast Sequencing Reports. A 12.8 kb segment, on the right arm of chromosome A:Reference number: S34925; MUID:93377417; PMID:8368014
 A:Accession: S34928
 A:Molecule type: DNA
 A:Residues: 91-352 <BU2>
 A:Cross-references: EMBL:Z21487
 C:Genetics:
 A:Gene: SGD:KTR3
 A:Cross-references: SGD:S0000409; MIPS:YBR205w
 A:Map position: 2R
 C:Keywords: transmembrane protein
 F:22-45/Domain: transmembrane #status predicted <TMM>

Query Match 8.9%; Score 91; DB 2; Length 404;
 Best Local Similarity 22.8%; Pred. No. 0.76; Mismatches 58; Indels 44; Gaps 5;
 Matches 36; Conservative 20

QY 35 SIHDDHKLVLDSGNIIVAVDKNYIRPE-----IFFALASSASAKGSPIL 84
 Db 2 SVH---HKKLMPSKALLIRKYGKIRSFITGLIYLSFFFGSGSRPEVPIAQTGTSV 58
 QY 85 LGVSKGEFCILYCDKDKQSHPSLQKKKELMLAAQKESARRPFIFRAQVSWNMLES 144
 Db 59 RVASKDYLMPTKSGQGVHVPDGRKKGAVYTLANS-----DLMLVKSI 106
 QY 145 AHPGWFCTSCNCEPEYGVTFDFENRKHIEFSF---OP 179
 Db 107 RH-----VEDRENRRHYDMVYLNQDP 128

RESULT 14
 JG5646
 Interleukin-1 beta - horse
 C:Species: Equus caballus (domestic horse)
 C>Date: 28-Oct-1997 #sequence, revision 28-Oct-1997 #text_change 20-Jun-2000
 C:Accession: JG5646
 R:Kato, H.; Yon, H.Y.; Ohashi, T.; Watarai, T.; Goltzuka, R.; Tsujimoto, H.; Hasegawa Gene 177, 11-16, 1996

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2003, 06:31:37 ; Search time 65 Seconds

(without alignments)
122.515 Million cell updates/sec

Title: US-09-876-790-3

Perfect score: 1017
Sequence: 1 MSGCDRRETFETKGNSEFKR.....IEFSFPVCKAMSPSEVSD 192

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	159	15.6	178	IL1X_MOUSE	P25085 bos musculus
2	152	14.9	174	IL1X_BOVIN	O77482 bos taurus
3	151.5	14.9	177	IL1X_RABIT	P26890 oryctolagus
4	149.5	14.7	177	IL1X_HUMAN	P18510 homo sapien
5	146.5	14.4	177	IL1X_PIG	O29056 sus scrofa
6	144.5	14.2	178	IL1X_PIG	P23086 sus scrofa
7	137.5	13.5	177	IL1X_HORSE	P18999 equus caball
8	129.5	12.5	267	IL1B_SHEEP	P21621 ovis aries
9	119.5	11.8	266	IL1B_PIG	P09428 bos taurus
10	112.5	11.1	266	IL1B_BOVIN	P79162 capra hircu
11	109.5	10.8	266	IL1B_BOVIN	O63284 ratu
12	107	10.5	268	IL1B_RAT	P51745 cervus elap
13	105	10.3	266	IL1B_CEREL	P10749 mus musculu
14	104	10.2	269	IL1B_MOUSE	O9x577 trichosurus
15	101	9.9	269	IL1B_TRIUV	O9wv91 cavia porce
16	98.5	9.7	266	IL1B_CAVPO	P01584 homo sapien
17	93	9.1	269	IL1B_HUMAN	O28386 equus cabal
18	92.5	9.1	268	IL1B_HORSE	P38130 saccharomyc
19	91	8.9	404	KTR3_YEAST	P41687 felis silve
20	89.5	8.8	267	IL1B_FELCA	P14628 oryctolagus
21	89	8.8	268	IL1B_RABIT	P46648 cercocebus
22	88.5	8.7	269	IL1B_CERTO	P48090 macaca mula
23	88.5	8.7	269	IL1B_MACMU	P56273 xenopus lae
24	88	8.7	473	MDM2_XENTLA	P51493 macaca neme
25	86	8.5	269	IL1B_MACNE	P01582 mus musculu
26	84	8.3	270	IL1A_MOUSE	O9wv77 ratu
27	84	8.3	2314	AKA6_RAR	P79182 macaca fasc
28	83.5	8.2	268	IL1B_MACFA	P50748 homo sapien
29	77	7.6	2209	Y166_HUMAN	O22226 caenorhabdi
30	76	7.5	425	Y194_CAREL	O22226 caenorhabdi
31	76	7.5	448	EXG1_YEAST	P23776 saccharomyc
32	76	7.5	501	C72N_ARATH	O91tm0 arabidopsis
33	74.5	7.3	256	YKJ9_YEAST	P34247 saccharomyc

ALIGNMENTS

RESULT 1	ID	IL1X_MOUSE	STANDARD:	PRT:	178 AA.
AC	P25085	O70207;			
DT	01-MAY-1992	(Rel. 22, Created)			
DT	01-MAY-1992	(Rel. 22, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)				
DE	(IRAP).				
GN	IL1RN OR IL-1RA.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_Taxid=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A. (ISOFORM 1)				
RA	MEDLINE=91250712; PubMed=1828262;				
RX	Zahedi K., Seidlin M.F., Rits M., Ezekowitz R.A., Whitehead A.S.;				
RT	"Mouse IL-1 receptor antagonist protein. Molecular characterization,				
RT	gene mapping, and expression of mRNA in vitro and in vivo."				
RL	J. Immunol. 146:4228-4233(1991).				
RN	[2]				
RP	SEQUENCE FROM N.A. (ISOFORM 1)				
RX	MEDLINE=91316273; PubMed=1830498;				
RA	Matsushima H., Roussel M.F., Matsushima K., Hishinuma A., Sherr C.J.;				
RT	"Cloning and expression of murine interleukin-1 receptor antagonist				
RT	in macrophages stimulated by colony-stimulating factor 1."				
RL	Blood 78:616-623(1991).				
RN	[3]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RC	STRAIN=Swiss;				
RX	MEDLINE=94271931; PubMed=8003626;				
RA	Zahedi K.A., Uhlar C.M., Rits M., Prada A.E., Whitehead A.S.;				
RT	"The mouse interleukin-1 receptor antagonist protein: gene structure				
RT	and regulation in vitro."				
RL	Cytokine 6:1-9(1994).				
RN	[4]				
RP	SEQUENCE FROM N.A. (ISOFORM 2).				
RC	STRAIN=FVB X DBA/1 JACF;				
RX	MEDLINE=98209757; PubMed=9550387;				
RA	Gabay C., Porter B., Fantuzzi G., Arend W.P.;				
RT	"Mouse IL-1 receptor antagonist isoforms: complementary DNA cloning				
RT	and protein expression of intracellular isoform and tissue				
RT	distribution of secreted and intracellular IL-1 receptor antagonist in				
RT	vivo."				
RL	J. Immunol. 159:5905-5913(1997).				
RN	[5]				
RP	SEQUENCE OF 7-178 FROM N.A.				
RX	MEDLINE=91271363; PubMed=1828896;				
RA	Bisenberg S.P., Brewer M.T., Verderber E., Heimdal P.;				
RT	Brandhuber B.J., Thompson R.C.;				
RT	"Interleukin 1 receptor antagonist is a member of the interleukin 1				
RT	gene family: evolution of a cytokine control mechanism."				
RL	Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).				
RN	[6]				
RP	SEQUENCE OF 23-178 FROM N.A.				

RA MEDLINE-92037824; PubMed-1834470;
 RA Shuck M.E., Bessalu T.E., Tracey D.E., Bienkowski M.J.;
 RT "Cloning, heterologous expression and characterization of murine
 RT Interleukin 1 receptor antagonist protein".
 RT Eur. J. Immunol. 21:2775-2780(1991).
 CC -1- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
 CC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: SECRETED (ISOFORM 1) OR INTRACELLULAR
 CC (ISOFORM 2).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
 CC produced by alternative splicing.
 CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M74294; AAA39309.1; -
 DR EMBL: M64404; AAA39277.1; -
 DR EMBL: L32838; AAA20576.1; -
 DR EMBL: AF001795; AAC15251.1; -
 DR EMBL: M57525; AAA39278.1; -
 DR EMBL: M63100; AAA39310.1; -
 DR EMBL: S64082; AAB20265.1; -
 DR PIR: B40956; B40956.
 DR PIR: A44610; A44610.
 DR HSSP: P18510; IL1R.
 DR MGD: MGI:96547; IL1rn.
 DR InterPro: IPR000975; Interleukin_1.
 DR Pfam: PF00340; IL1; 2.
 DR ProDom: PD002536; Interleukin_1; 1.
 DR SMART: SM00125; IL1; 1.
 DR PROSITE: PS00253; INTERLEUKIN_1; 1.
 DR KEGG: Glycoprotein; Signal; Alternative splicing.
 FT SIGNAL 1 26 BY SIMILARITY.
 FT CHAIN 27 178 INTERLEUKIN-1 RECEPTOR ANTAGONIST
 FT PROTEIN.
 FT DISULFID 92 142 BY SIMILARITY.
 FT CARBOHYD 110 110 N-LINKED (GLCNAC...) (POTENTIAL).
 FT VARSPLIC 1 21 MEICMGPSHLSISLLILLFH -> MA (IN ISOFORM
 FT 2)
 SQ SEQUENCE 178 AA: 20274 MW: 84AA002A3119C024 CRC64;
 Query Match 15.6%; Score 159; DB 1; Length 178;
 Best Local Similarity 32.7%; Pred. No. 2,7e-08;
 Matches 48; Conservative 23; Mismatches 64; Indels 12; Gaps 7;
 QY 34 FSIHDDHKVLVDSGNLIAPDKNYIR-PEIFPALASSLSASAENKSPILLGVSGEEF 92
 DB 39 FRIMVTNOKTYFLRNNOILIA---GYLOGPNI--KLEEKIMVPIDILHS-VFLGIHGKGL 91
 QY 93 CLYCDKDGQSHPSLOLTKKELMKLAQKESARPFIFRAQVSWMNLLEAHPGFIC 152
 DB 92 CLSCAKSSDDI--KLQLEEVNITDLSKKNEDKR-FTFIREKPTTSFESAACPWFLLC 148
 QY 153 TSCNCPNEPVGYDKFENRKH-IEFSFQ 178
 DB 149 TLEADRPVSLNTPPEELVTKYFQ 175
 RESULT 2
 ID IL1X_BOVIN STANDARD; PRT; 174 AA.
 AC 077482;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
 DE (IRAP).

GN IL1RN.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-98305607; PubMed-9643454;
 RA Kiritawa R., Fukuda T., Yamana H., Hagiwara K., Goto M., Ohta Y.,
 RA Yoshino T., Iwai H.;
 RT "Enzymatic amplification and expression of bovine Interleukin-1
 RT receptor antagonist cDNA".
 RL Vet. Immunol. Immunopathol. 62:197-208(1998).
 CC -1- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
 CC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
 CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AB005148; BAA31854.1; -
 DR HSSP: P18510; IL1R.
 DR InterPro: IPR000975; Interleukin_1.
 DR Pfam: PF00340; IL1; 1.
 DR ProDom: PD002536; Interleukin_1; 1.
 DR SMART: SM00125; IL1; 1.
 DR PROSITE: PS00253; INTERLEUKIN_1; 1.
 DR KEGG: Glycoprotein; Signal.
 FT SIGNAL 1 23 BY SIMILARITY.
 FT CHAIN 24 174 INTERLEUKIN-1 RECEPTOR ANTAGONIST
 FT PROTEIN.
 FT DISULFID 89 139 BY SIMILARITY.
 FT CARBOHYD 107 107 N-LINKED (GLCNAC...) (POTENTIAL).
 FT VARSPLIC 1 174 ME56E7P224FF851F CRC64;
 SQ SEQUENCE 174 AA: 19926 MW: 1E56E7P224FF851F CRC64;
 Query Match 14.9%; Score 152; DB 1; Length 174;
 Best Local Similarity 29.6%; Pred. No. 1.2e-07;
 Matches 48; Conservative 18; Mismatches 54; Indels 42; Gaps 6;
 QY 34 FSIHDDHKVLVDSGNLIAPDKNYIR-PEIFPALASSLSASA 77
 DB 36 FRIMDVNOKTFEYLRNNOVLVAGYLOGPNTKLEKIDVP---IEPHTMF----- 80
 QY 78 EKSPILLGVSKGEFLCYCDKDGQSHPSLOLTKKELMKLAQKESARPFIFRAQVS 137
 DB 81 -----LGIHGKGLCLACVKSQDEI--KLKLEAVNITDLNQREDDKR-FAFIRFDNCP 130
 QY 138 WMNLESAHPGWGFTSCNCPNEPVGYTD-KFEKRKHIEFSFQ 178
 DB 131 TTFESAPCPGFWLCTSLADQPVGLTNMPTALKVTKYFQ 172
 RESULT 3
 ID IL1X_RABIT STANDARD; PRT; 177 AA.
 AC P26890;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
 DE (IRAP).
 GN IL1RN OR IL1RA.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxID=9986;
 RN [1]

SEQUENCE FROM N.A.
 MEDLINE=94165101; PubMed=7509813;
 RA Cominelli F., Bortolami M., Pizzaro T.T., Monsacchi L., Ferretti M.,
 RA Brewer M.T., Eisenberg S.P., Ng R.K.,
 RT "Rabbit interleukin-1 receptor antagonist. Cloning, expression,
 RT functional characterization, and regulation during intestinal
 RT inflammation.";
 RL J. Biol. Chem. 269:6962-6971(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Hamada H., Mulligan R.C.;
 RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93052512; PubMed=1427977;
 RA Goto F., Goto K., Miyata T., Ohkawa S., Takao T., Mori S.,
 RA Furukawa S., Maeda T., Iwanaga S., Shimomishi Y., Yoshihaga M.;
 RT "Interleukin-1 receptor antagonist in inflammatory exudate cells of
 RT rabbits. Production, purification and determination of primary
 RT structure.";
 RL Immunology 77:235-244(1992).
 CC -1- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
 CC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
 CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: S68977; AAB30093.1; -
 DR EMBL: M57526; AAA31374.1; -
 DR EMBL: D21832; AAA04860.1; -
 DR PIR: A54377; A54377.
 DR HSSP: P18510; IILR.
 DR InterPro: IPR000975; Interleukin_1.
 DR Pfam: PF00340; IL1; 1.
 DR ProDom: PD002536; Interleukin_1; 1.
 DR SMART: SM00125; IL1; 1.
 DR PROSITE: PS00253; INTERLEUKIN_1; 1.
 KW Glycoprotein; Signal.
 FT SIGNAL 1 25
 FT CHAIN 26 177
 FT DISULFID 91 141
 FT CARBOHYD 109 109
 FT SEQUENCE 177 AA; 20214 MW; F5BC08F097FEAF CRC64;
 SO
 Query Match 14.9%; Score 151.5; DB 1; Length 177;
 Best Local Similarity 26.9%; Pred. No. 1.4e-07;
 Matches 47; Conservative 25; Mismatches 50; Indels 53; Gaps 7;
 QY 9 TETGKNSFKRLGPKYKNIINPKKESIHDHDKVILVDSGNLIA----- 53
 DB 21 SETCRBGRGKRCR-----MQAFRIWVNOKTFYLRNNOIYAGYLQGPNAKLEBRID 72
 QY 54 -VPPKNYIRPEIFPALASSLSASAEKGPILLGVSGEPCLYCDK--DDGSHPSIQLK 110
 DB 73 VVP-----LEPQLLF-----LGIQNGKLCCLSCVSKGDKMKLH---LE 106
 QY 111 KEKIMLAQKESARPFIFRYRAQVGMNMLESAHGFICTSCNCEPVGYVD 165
 DB 107 AVNITDLGKNEQDKR-FTFIRSNSGPTTFESASCGWFLCALADQVYSULN 160
 RESULT 4
 IL1X_HUMAN STANDARD; PRT; 177 AA.
 ID IL1X_HUMAN
 AC P18510; Q14628; Q9UPC0;
 DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Interleukin-1 receptor antagonist protein precursor (IL-1RA) (ICIL-
 DE IRA) (IRAP) (IL-1RN).
 GN IL1RN OR IL1RA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=90220867; PubMed=2139180;
 RA Carter D.B., Deibel M.R., Jr., Dunn C.J., Tomich C.S.C., Laborde A.L.,
 RA Slightom J.L., Berger A.E., Bienkowski M.J., Sun F.F., McEwan R.N.,
 RA Harris P.K.W., Yem A.W., Waszak G.A., Chosay J.G., Siew L.C.,
 RA Hardee M.M., Zurcher-Neely H.A., Reardon I.M., Heindrickson R.L.,
 RA Truesdell S.E., Shelly J.A., Bessatsu T.E., Taylor B.M., Tracey D.E.;
 RT "Purification, cloning, expression and biological characterization of
 RT an interleukin-1 receptor antagonist protein.";
 RL Nature 344:633-638(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=90136921; PubMed=2137201;
 RA Eisenberg S.P., Evans R.J., Arend W.P., Verderber E., Brewer M.T.,
 RA Hannum C.H., Thompson R.C.;
 RT "Primary structure and functional expression from complementary DNA
 RT of a human interleukin-1 receptor antagonist.";
 RL Nature 343:341-346(1990).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=91271363; PubMed=1828896;
 RA Eisenberg S.P., Brewer M.T., Verderber E., Heindal P.,
 RA Brandhuber B.J., Thompson R.C.;
 RT "Interleukin 1 receptor antagonist is a member of the interleukin 1
 RT gene family: evolution of a cytokine control mechanism.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=92338323; PubMed=185987;
 RA Lennard A., Gotman P., Carrier M., Griffiths S., Scotney H.,
 RA Sheer D., Solari R.;
 RT "Cloning and chromosome mapping of the human interleukin-1 receptor
 RT antagonist gene.";
 RL Cytokine 4:83-89(1992).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
 RX MEDLINE=97146044; PubMed=892991;
 RA Arend W.P., Drono R.F., Shuck M.E., Bienkowski M.J., Slightom J.L.,
 RA Jaffe G.J., Hammerberg C., Sporn S.A., Fong S., Arend W.P., Ralph P.;
 RT "Intracellular IL-1 receptor antagonist promoter: cell type-specific
 RT and inducible regulatory regions.";
 RL J. Immunol. 158:748-755(1997).
 RN [6]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=91219436; PubMed=1827201;
 RA Haskell S., Martin G., Van Le L., Morris J., Peace A., Bigler C.F.,
 RA Jaffe G.J., Hammerberg C., Sporn S.A., Fong S., Arend W.P., Ralph P.;
 RT "cDNA cloning of an intracellular form of the human interleukin 1
 RT receptor antagonist associated with epithelium.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:3681-3685(1991).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RX MEDLINE=95355865; PubMed=762950;
 RA Muzio M., Polentarutti N., Sironi M., Poli G., De Giola L.,
 RA Introna M., Mantovani A., Colotta F.;
 RT "Cloning and characterization of a new isoform of the interleukin 1
 RT receptor antagonist.";
 RL J. Exp. Med. 182:623-628(1995).
 RN [8]
 RP SEQUENCE OF 26-45.
 RX MEDLINE=90136920; PubMed=2137200;
 RA Hannum C.H., Wilcox C.J., Arend W.P., Joslin F.G., Dripps D.J.,
 RA Heindal P.L., Armes L.G., Sommer A., Eisenberg S.P., Thompson R.C.;

```

RT      "Interleukin-1 receptor antagonist activity of a human interleukin-1
RT      inhibitor." ;
RT      Nature 343:336-340(1990) .
RN      [9]
RN      SEQUENCE OF 26-52.
RX      MEDLINE-90354444; PubMed-2143761;
RA      Blankowski M.J., Eessalu T.E., Berger A.E., Truesdell S.E.,
RA      Shelly J.A., Laborde A.L., Zucher-Nelly H.A., Reardon I.M.,
RA      Helmlison R.L., Chosay J.G., Tracey D.B.;
RT      "Purification and Characterization of Interleukin 1 receptor level
RT      antagonist proteins from THP-1 cells." ;
RL      J. Biol. Chem. 265:14505-14511(1990).
RN      [10]
RN      SEQUENCE OF 35-177 FROM N.A. (ISOFORM 4).
RX      MEDLINE-98183404; PubMed-9514884;
RA      Weissbach L., Tran K., Colquhoun S.A., Champilaud M.F., Towle C.A.;
RT      "Detection of an Interleukin-1 Intracellular Receptor Antagonist mRNA
RT      Variant." ;
RL      Biochem. Biophys. Res. Commun. 244:91-95(1998).
RN      [11]
RN      STRUCTURE BY NMR.
RX      MEDLINE-92297633; PubMed-1534997;
RA      Stockman B.J., Scallill T.A., Roy M., Ulrich E.L., Strakalaitis N.A.,
RA      Brunner D.P., Yem A.W., Deibel M.R. Jr.;
RT      "Secondary structure and topology of interleukin-1 receptor
RT      antagonist protein determined by heteronuclear three-dimensional NMR
RT      spectroscopy." ;
RL      Biochemistry 31:5237-5244(1992).
RN      [12]
RN      STRUCTURE BY NMR.
RX      MEDLINE-94320651; PubMed-8045306;
RA      Stockman B.J., Scallill T.A., Strakalaitis N.A., Brunner D.P.,
RA      Yem A.W., Deibel M.R. Jr.;
RT      "Solution structure of human interleukin-1 receptor antagonist
RT      protein." ;
RL      FEBS Lett. 349:79-83(1994).
RN      [13]
RN      X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX      MEDLINE-94230368; PubMed-8175703;
RA      Vigers G.P.A., Caffes P., Evans R.J.J., Thompson R.C., Eisenberg S.P.,
RA      Brandhuber B.J.;
RT      "X-ray structure of interleukin-1 receptor antagonist at 2.0-A
RT      resolution." ;
RL      J. Biol. Chem. 269:12874-12879(1994).
RN      [14]
RN      X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX      MEDLINE-95172072; PubMed-7867645;
RA      Schneider H.A., Rondeau J.-M., Tardif C., Soffientini A., Sarubbi E.,
RA      Aksos A., Bowlin T.L., Yanofsky S., Barrett R.W.;
RT      "Refined crystal structure of the Interleukin-1 receptor antagonist.
RT      Presence of a disulfide link and a cis-proline." ;
RL      Eur. J. Biochem. 227:838-847(1995).
RN      [15]
RN      X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 32-177 IN COMPLEX WITH IL1R.
RX      MEDLINE-97215904; PubMed-9062194;
RA      Schneider H., Tardif C., Trump-Kallmeyer S., Soffientini A.,
RA      Sarubbi E., Aksos A., Bowlin T., Yanofsky S., Barrett R.W.;
RT      "A new cytokine-receptor binding mode revealed by the crystal
RT      structure of the IL-1 receptor with an antagonist." ;
RL      Nature 386:194-200(1997).
CC      -1- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC      RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC      -1- SUBCELLULAR LOCATION: SECRETED (ISOFORM 1) OR INTRACELLULAR
CC      (ISOFORMS 2, 3 AND 4) .
CC      -1- ALTERNATIVE PRODUCTS: 4 isoforms: 1 (shown here), 2/ilc1-1ra,
CC      3/ilc1-1ra type II and 4; are produced by alternative splicing.
CC      -1- TISSUE SPECIFICITY: THE INTRACELLULAR FORM OF IL-1RA IS
CC      PREDOMINANTLY EXPRESSED IN EPITHELIAL CELLS.
CC      -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC      -1- DATABASE: NAME=R&D Systems' cytokine source book; IL1RN;
CC      WWW="http://www.rndsystems.com/asp/9_slebuilder.asp?bodyId=205" .
CC      This SWISS-PROT entry is copyright It is produced through a collaboration
CC      -----

```

```

CC      between the Swiss Institute of Bioinformatics and the EMBL outstation
CC      The European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; M55646; AAA59138.1; -
DR      EMBL; M63099; AAB41943.1; -
DR      EMBL; X52015; CA36262.1; -
DR      EMBL; X53296; CA37386.1; -
DR      EMBL; X64532; CAA45832.1; -
DR      EMBL; U65590; AAB92268.1; -
DR      EMBL; U65590; AAB92270.1; -
DR      EMBL; X84348; CAA59087.1; -
DR      EMBL; U65590; AAB92269.1; -
DR      EMBL; AF043143; AAC39672.1; -
DR      PIR; A30368; A30368.
DR      PIR; A37822; A37822.
DR      PIR; S08160; S08160.
DR      PIR; S08159; S08159.
DR      PIR; A40956; A40956.
DR      PIR; A39386; A39386.
DR      PDB; 1ITT; 30-APR-94.
DR      PDB; 2IRT; 15-OCT-94.
DR      PDB; 1IRT; 27-FEB-95.
DR      PDB; 1ILR; 07-FEB-95.
DR      PDB; 1ILT; 01-APR-95.
DR      PDB; 1IRA; 17-JUN-98.
DR      Aarhus/Ghent-2DPAGE; 7104; IEF.
DR      Aarhus/Ghent-2DPAGE; 7105; IEF.
DR      Genew; HGNC:6000; IL1RN.
DR      MIM; 147679; -.
DR      InterPro; IPR000975; Interleukin_1.
DR      Pfam; PF00340; IL1; 3.
DR      ProDom; PPD002536; Interleukin_1; 1.
DR      SMART; SM00125; IL1; 1.
DR      PROSITE; PS00253; INTERLEUKIN_1; 1.
KW      Glycoprotein; Signal; Alternative splicing; 3D-structure.
FT      SIGNAL 1 25
FT      CHAIN 26 177 INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT      PROTEIN.
FT      DISULFD 91 141 N-LINKED (GLCNAC... ) (POTENTIAL).
FT      CARBOHD 109 109 MEIOGRSLHILITLLFLFHS -> MAL (IN
FT      VARSPLIC 1 21 ISOFORM 2) .
FT      VARSPLIC 1 21 MEIOGRSLHILITLLFLFHS -> MALADYEBGGGGGE
FT      VARSPLIC 1 21 GEDNDSK (IN ISOFORM 3) .
FT      VARSPLIC 1 34 GEDNDSK (IN ISOFORM 4) .
FT      SEQUENCE 177 AA; 20055 MW; D1690776A7394057 CAC64;
SQ
Query Match 14.7%; Score 149.5; DB 1; Length 177;
Best Local Similarity 29.3%; Pred. No. 2.2e-07;
Matches 41; Conservative 28; Mismatches 60; Indels 11; Gaps 6;
QY 27 KNLNKKKSIHQDHQKVLVDGSLNLAVPDKNYIR-PEIIFPLASSLSASAKSGSPILL 85
DB 31 KSSKKQARFIMVYNOKSTFTYLRNNQILVA-----GYLOGPNV--NLEEKIDVPIEPHA-LFL 83
QY 86 GYSKGEFCLCYCDKDKDGSHPSLOLKKKELMKLAAQESARREPIFYRAQVGSMMNLIESNA 145
DB 84 GIHGKMKCLCVKSGSDETR-LQLBAVNITDLSENRKQDKR-FAIRSDSGPTTSFESAA 140
QY 146 HPGWFICTSCNENPEVGYTD 165
DB 141 CPGWELCTAMEADQPVSLTN 160
RESULT 5
IL1X_PIG STANDARD; PRT; 177 AA.
AC Q29056;
DT 15-DEC-1998 (Rel. 37, Created)

```

```

DT 15-DEC-1998 (Rel. 37, Last sequence update)
DR 15-JUL-1999 (Rel. 38, Last annotation update)
DE Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
GN (IRAP).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Crossbred; TISSUE=Lung;
RA Yin J., Murtaugh M.P.;
RT "Characterization of IRAP in morphine treated pigs.";
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L38849; AAA99424.1; -
DR HSSP; P18510; IL1RA.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
DR Glycoprotein; Signal.
FT CHAIN 1 25 BY SIMILARITY.
FT SIGNAL 1 25 INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT FT PROTEIN.
FT DISULFID 91 141 BY SIMILARITY.
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 177 AA; 20093 MW; 2114DC6119A9D5F9 CRC64;

Query Match 14.4%; Score 146.5; DB 1; Length 177;
Best Local Similarity 28.4%; Pred. No. 4.3e-07;
Matches 42; Conservative 16; Mismatches 49; Indels 41; Gaps. 5;

QY 34 FSIHDDHKVLYVDSGNLIA-----VPDKNYIRPELFFALSSLSASA 77
DB 38 FRIMDVNOKFTYLRNNQVAGYLOGPNTKLEKIDVFP-----VEPHVF----- 82
QY 78 EKGSPILGVSKGEFCYCDKDGQSHPSLOLKEKIMKLAOKESARPPFIYRAOVGS 137
DB 83 -----LGIHGKILCLSCVKSDEM--KLQLDVAVNITDLKRNSEQDKR-FTFRSDSGP 132

QY 138 WNMLESAAHPGWFCTSCNCEPVGVD 165
DB 133 TTSPESACPEWFLCTALDEADPGVLTN 160

RESULT 6
IL1X_RAT STANDARD; PRT; 178 AA.
AC P25086;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE (IRAP).
GN IL1RN OR IL-1RA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=91271363; PubMed=1828896;
RA Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
RA Brandhuber B.J., Thompson R.C.;
RT "Interleukin 1 receptor antagonist is a member of the interleukin 1
RT gene family: evolution of a cytokine control mechanism.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
CC -1- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M63101; AAA1434.1; -
DR PIR; C40956; C40956.
DR HSSP; P18510; IL1R.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
DR Glycoprotein; Signal.
FT CHAIN 1 26 BY SIMILARITY.
FT SIGNAL 1 26 INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT FT PROTEIN.
FT DISULFID 92 142 BY SIMILARITY.
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 178 AA; 20282 MW; F3A5734FB6C51B03 CRC64;

Query Match 14.2%; Score 144.5; DB 1; Length 178;
Best Local Similarity 29.1%; Pred. No. 6.7e-07;
Matches 41; Conservative 20; Mismatches 53; Indels 27; Gaps 4;

QY 34 FSIHDDHKVLYVDSGNLIA-----VPDKNYIRPELFFALSSLSASA 84
DB 39 FRIMDVNOKFTYLRNNQVAGYLOGPNTKLEKIDVFPIDF-----RNVF 83
QY 85 LGVSKGEFCYCDKDGQSHPSLOLKEKIMKLAOKESARPPFIYRAOVGSWNMTESA 144
DB 84 LGIHGKILCLSCVKSDDT--KLQLEEVNITDLNKKEDKR-FTFRSETPTTFSFSL 140
QY 145 AHPGWFCTSCNCEPVGVD 165
DB 141 ACPGWFCTTLEADHPVSLTN 161

RESULT 7
IL1X_HORSE STANDARD; PRT; 177 AA.
AC O18999; O77745;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE (IRAP).
GN IL1RN OR IL1RA.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=97366446; PubMed=9223227;
RA Kato H., Ohashi T., Matsushiro H., Watarai T., Goitsuka R.,
RA Tsujimoto H., Hasegawa A.;
RT "Molecular cloning and functional expression of equine interleukin-1

```

```

RT receptor antagonist."
RL Vet. Immunol. Immunopathol. 56:221-231(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-98285942; PubMed-9622739;
RA Howard R.D., McIlwraith C.W., Trotter G.W., Nyborg J.K.;
RT "Cloning of equine interleukin-1 receptor antagonist and
RL determination of its full-length cDNA sequence."
RL Am. J. Vet. Res. 59:712-716(1998).
CC -1- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D83714; BAA2529.1;
DR EMBL: U92482; AAC39257.1;
DR HSSP: P18510; ILIR.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR ProDom: PD002536; Interleukin_1; 1.
DR SMART: SM00125; IL1; 1.
DR PROSITE: PS00253; INTERLEUKIN_1; 1.
DR KEGG: Glycylproteins; Signal.
FT SIGNAL 1 25
FT CHAIN 26 177 BY SIMILARITY.
FT INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT PROTEIN.
FT DISULFID 91 141 BY SIMILARITY.
FT CARDHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 19 19 F -> L (IN REF. 2).
SQ SEQUENCE 177 AA; 20459 MW; 1ABC377F1FC80B CRC64;

Query Match 13.5%; Score 137.5; DB 1; Length 177;
Best Local Similarity 30.1%; Pred. No. 3.2e-06;
Matches 40; Conservative 22; Mismatches 62; Indels 9; Gaps 5;

OY 34 FSIHDDHVLVDGSLNLAVPDKNYIREIFALASSSSAASKGSPILLGVSKGPC 93
DB 38 FRIMDVNQTFTYRNNOVA---GLQ-ESNFKIQEKIDVPIPPDA-LFGGLGRKLC 91
OY 94 LYCDKDGQSHPSLQLKKEKLMKLAOKESARRPFIFYRAQVGSNNMLESAAHPGMFICT 153
DB 92 LACVKSQGEIR--FOLEAVNITDLSKNKRNKR-FTFIRNSGPTTSESAAACPGMFICT 148
OY 154 SCNCNEPVCVTDK 166
DB 149 AQEADRPVSLTNK 161

RESULT 8
IL1B_SHEEP
ID IL1B_SHEEP STANDARD: PRT; 266 AA.
AC P21621;
DR 01-MAY-1991 (Rel. 18, Created)
DR 01-MAY-1992 (Rel. 21, Last sequence update)
DR 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-1 beta precursor (IL-1 Beta).
GN IL1B.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_Taxid=9940;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE-92119335; PubMed-1840515;
RA Seow H.F., Rothel J.S., David M.J., Wood P.R.;

```

```

RT "Nucleotide sequence of ovine macrophage interleukin-1 beta cDNA."
RL DNA Seq. 1:423-426(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-91088326; PubMed-2263490;
RA Fiskerstrand C., Sargan D.;
RT "Nucleotide sequence of ovine interleukin-1 beta."
RL Nucleic Acids Res. 18:7165-7165(1990).
CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -1- SUBUNIT: MONOMER.
CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -----
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X54796; CAA38566.1;
DR EMBL: X56972; CAA40293.1;
DR PIR: S13092; S13092.
DR PIR: S13810; S13810.
DR PIR: S23010; S23010.
DR HSSP: P01584; STIB.
DR InterPro: IPR002348; IL1_HBGF.
DR InterPro: IPR003502; IL1_propep.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR Pfam: PF02394; IL1_propep; 1.
DR PRINTS: PR00262; IL1HBGF.
DR ProDom: PD002536; Interleukin_1; 1.
DR SMART: SM00125; IL1; 1.
DR PROSITE: PS00253; INTERLEUKIN_1; 1.
DE Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 113
FT CHAIN 114 266 INTERLEUKIN-1 BETA.
FT CONFLICT 14 14 Y -> C (IN REF. 2).
FT CONFLICT 55 55 Q -> K (IN REF. 2).
FT CONFLICT 64 64 V -> A (IN REF. 2).
FT CONFLICT 145 145 P -> L (IN REF. 2).
SQ SEQUENCE 266 AA; 30717 MW; BDED07B58224AB78 CRC64;

Query Match 12.5%; Score 127.5; DB 1; Length 266;
Best Local Similarity 29.5%; Pred. No. 4.8e-05;
Matches 39; Conservative 26; Mismatches 58; Indels 9; Gaps 6;

OY 33 KFSIHDDHVLVDG---NLAVPDKNYIREIFALASSSSAASKGSPILLGVSK 89
DB 120 KCKIQDEQKSLVDSCVLAHLPSQEMSR-EVVFQCM-SFVQGERDKKIPVALGIRD 177
OY 90 GEFCLYCDKDGQSHPSLQLKKEKLMKLAOKESARRPFIFYRAQVGSNNMLESAAHPGM 149
DB 178 KNYLSGVK-KGDT-PIQL--EVDPKVYPRKMKREKRVFTETKNTVFEFSVLYPWW 233
OY 150 FICTSCNCNEPV 161
DB 234 YISTSQTEERPV 245

RESULT 9

```

IL1B_PIG STANDARD; PRT; 267 AA.
 ID IL1B_PIG
 AC P26889;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Interleukin-1 beta precursor (IL-1 beta).
 GN IL1B.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxID=9823;
 RX MEDLINE=93314975; PubMed=8325511;
 RA Hether M.J., Lin G., Smith D.M., Murtaugh M.P., Mollitor T.W.;
 RT "Cloning, sequencing and regulation of an mRNA encoding porcine
 Interleukin-1 beta."
 RL Gene 129:285-289(1993).
 CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
 THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
 MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
 CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
 CC -1- SUBUNIT: MONOMER.
 CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
 CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
 CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
 CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
 CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
 CC SECRETORY PROTEINS.
 CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M86725; AAA02584.1; -
 DR PIR; JN0724; JN0724.
 DR HSSP; P01584; 1HIB.
 DR InterPro: IPR002348; IL1_HBGF.
 DR InterPro: IPR003502; IL1_PROPEP.
 DR InterPro: IPR000975; Interleukin_1.
 DR Pfam; PF00340; IL1; 1.
 DR Pfam; PF02394; IL1_PROPEP; 1.
 DR PRINTS; PR00262; IL1HBGF.
 DR PRODOM; PD002536; Interleukin_1; 1.
 DR SMART; SM00125; IL1; 1.
 DR PROSITE; PS00253; INTERLEUKIN_1; 1.
 DR Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
 KW PROPEP
 FT CHAIN 1 114 BY SIMILARITY.
 FT CHAIN 115 267 INTERLEUKIN-1 BETA.
 FT SEQUENCE 267 AA; 30404 MW; 7F6B92B784D5086F CRC64;
 Query Match 11.8%; Score 119.5; DB 1; Length 267;
 Best Local Similarity 27.0%; Pred. No. 0.00028;
 Matches 37; Conservative 27; Mismatches 64; Indels 9; Gaps 5;

DB 230 LYPNWTSTSOAEOKPV 246
 RESULT 10
 ID IL1B_BOVIN STANDARD; PRT; 266 AA.
 AC P09428;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Interleukin-1 beta precursor (IL-1 beta).
 GN IL1B.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 RX MEDLINE=89016591; PubMed=3262866;
 RA Leong S.R., Plaggs G.M., Lawman M., Gray P.W.;
 RT "The nucleotide sequence for the cDNA of bovine interleukin-1 beta."
 RL Nucleic Acids Res. 16:9054-9054(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88318652; PubMed=3261832;
 RA Maliszewski C.R., Baker P.E., Schoenborn M.A., Davis B.S., Cosman D.,
 RA Gillis S., Cerretti D.P.;
 RT "Cloning, sequence and expression of bovine interleukin 1 alpha and
 RT Interleukin 1 beta complementary DNAs."
 RL Mol. Immunol. 25:429-437(1988).
 CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
 CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
 CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
 CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
 CC -1- SUBUNIT: MONOMER.
 CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
 CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
 CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
 CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
 CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
 CC SECRETORY PROTEINS.
 CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M35589; AAA30585.1; -
 DR EMBL; X12498; CAA31018.1; -
 DR EMBL; M37211; AAA30584.1; -
 DR PIR; J10010; ICB01B.
 DR PIR; S01380; S01380.
 DR HSSP; P01584; 1HIB.
 DR InterPro: IPR002348; IL1_HBGF.
 DR InterPro: IPR003502; IL1_PROPEP.
 DR InterPro: IPR000975; Interleukin_1.
 DR Pfam; PF00340; IL1; 1.
 DR Pfam; PF02394; IL1_PROPEP; 1.
 DR PRINTS; PR00262; IL1HBGF.
 DR PRODOM; PD002536; Interleukin_1; 1.
 DR SMART; SM00125; IL1; 1.
 DR PROSITE; PS00253; INTERLEUKIN_1; 1.
 DR Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
 KW PROPEP
 FT CHAIN 1 113
 FT CHAIN 114 266 INTERLEUKIN-1 BETA.
 FT CHAIN 267
 FT CONFLICT 252 252 A -> G (IN REF. 2).
 FT

KW PROSITE:PS00253; INTERLEUKIN_1.1.
 RW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
 FT PROPER 1 113 BY SIMILARITY.
 FT CHAIN 114 266 INTERLEUKIN-1 BETA.
 SQ SEQUENCE 266 AA; 30/69 MW; 59F7B39BD1D4DDA5 CRC64;
 Query Match 10.8%; Score 109.5; DB 1; Length 266;
 Best Local Similarity 26.7%; Pred. No. 0.0026;
 Matches 35; Conservative 25; Mismatches 64; Indels 7; Gaps 4;
 QY 33 KFSIHDDHKVLYLDSGNLIAPVD--KATYRPEIFPALASSLSASAEKSPILLGVSG 90
 Db 120 KCTLIQDRKQSLTVLSPCYLKAHLHLSQEMSEREVFCM-SFVGGEERDNKIPALDIRDK 178
 QY 91 EPCLYCDKQKQSGHPELQJLKEKLEKLKLAQKESARPFIFPRVAVGSMNLSAHPGWF 150
 Db 179 N-LYLSWVKKGGTPIQL--EVDQPKYPRPNRNEKFEVYKTEIKNTYFESEVLPRNY 234
 QY 151 ICTSCNCEPV 161
 Db 235 ISTQIEKPV 245
 RESULT 12
 IL1B_RAT STANDARD: PRT; 268 AA.
 ID IL1B_RAT
 AC 063264;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Interleukin-1 beta precursor (IL-1 beta).
 GN IL1B.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE-Macrophage;
 RA Fresser W., Fremark B.D.;
 RL Submitted (Aug-1992) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
 CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
 CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
 CC DECRYPTERED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
 CC -1- SUBUNIT: MONOMER.
 CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
 CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
 CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
 CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
 CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
 CC SECRETORY PROTEINS.
 CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
 CC
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb.ch/announce/>
 CC or send an email to license@isb.ch).
 CC
 CC EMBL: M98820; AAA1426.1; -
 CC HSSP: P10749; 2MTB.
 DR Interpro: IPR002348; IL1_HBGF.
 DR Interpro: IPR003502; IL1_PROPEP.
 DR Interpro: IPR000975; Interleukin_1.
 DR Pfam: PF00340; IL1; 1.
 DR Pfam: PF02394; IL1_propep; 1.
 DR PRINTS: PRO0262; IL1HBGF.
 DR ProDom: PD002356; Interleukin_1; 1.
 DR


```
CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
```

DR EMBL; M15131; AAA39276.1; -
DR EMBL; X04964; CAA28637.1; -
DR PIR; A24719; A24719.
DR PIR; S13029; S13029.
DR PDB; 811B; 15-OCT-94.
DR PDB; 2MB; 31-JAN-94.
DR MGD; MGI:96543; 111b.
DR InterPro; IPR002348; IL1_HBGF.
DR InterPro; IPR003502; IL1_propep.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1_1.
DR Pfam; PF02394; IL1_propep; 1.
DR PRINTS; PR00262; IL1HBGF.
DR PRODOM; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1_1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen;
KW 3d-structure.
FT PROPEP 1 117
FT CHAIN 118 269 INTERLEUKIN-1 BETA.
FT STRAND 123 129
FT TURN 130 131
FT STRAND 134 137
FT TURN 140 141
FT STRAND 143 146
FT TURN 150 154
FT STRAND 163 163
FT TURN 170 171
FT STRAND 173 179
FT TURN 180 181
FT STRAND 184 191
FT TURN 192 193
FT STRAND 194 201
FT TURN 204 206
FT HELIX 214 216
FT STRAND 217 222
FT STRAND 227 231
FT TURN 235 236
FT STRAND 242 248
FT STRAND 247 248
FT STRAND 250 252
FT STRAND 258 259
FT STRAND 262 266
SQ SEQUENCE 269 AA; 734FAL7B02EDB7EE CRC64;

Query Match 10.2%; Score 104; DB 1; Length 269;
Best Local Similarity 27.5%; Pred. No. 0.0089;
Matches 41; Conservative 29; Mismatches 71; Indels 8; Gaps 6;

QY 34 FSIHDDHVLVLT-DSGNLAVP-DKNYTRPEIFALASSLSASAEKSPILLGVSGE 91
DB 125 YILRDEQKQSLVSDPYELKALHLNGQINQVITSMSEVQCEPSNDK-IPVALGLCKGN 183
QY 92 FCLYCDKDKGQSHPSLQKKERLMLAAQESARRPFIFYRAOVGSMMMLSSAAPGWFI 151
DB 184 LVLSGVMKDG-PTLQL-ESVDPKQYPRKKMKERFVNFKIEVASKVEFESAEFPNMYI 239

```
QY 152 CTSCNCEPVGVDKFNKRKHIEFSPQV 180  
DB 240 STSQAEHRKVPFLGN-SGQDIIDFIMESV 267  
RESULT 15  
ID IL1B_TRIUV STANDARD; PRT; 269 AA.  
AC 09XS77;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Interleukin-1 beta precursor (IL-1 beta).  
GN IL1B.  
OS Trichosurus vulpecula (Brush-tailed possum).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.  
OX NCBI_Taxid=9337;  
RN 1  
RP MEDLINE-99221044; PubMed-10206203;  
RA Wedlock D.N., Goh L.P., Parlane N.A., Buddle B.M.;  
RT "Molecular cloning and physiological effects of Drushtail possum  
RT Interleukin-1beta."  
RL Vet. Immunol. Immunopathol. 67:359-372(1999).  
CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES  
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL  
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.  
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING  
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE  
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.  
CC -1- SUBUNIT: MONOMER.  
CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE  
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.  
CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE  
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS  
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER  
CC SECRETORY PROTEINS.  
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.  
CC -----  
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
```

DR EMBL; AF071539; AAD21871.1; -
DR HSSP; P01584; IAI1.
DR InterPro; IPR002348; IL1_HBGF.
DR InterPro; IPR003502; IL1_propep.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1_1.
DR Pfam; PF02394; IL1_propep; 1.
DR PRINTS; PR00262; IL1HBGF.
DR PRODOM; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1_1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
KW PROPEP 1 112
KW CHAIN 113 269 INTERLEUKIN-1 BETA.
FT STRAND 112 112
SQ SEQUENCE 269 AA; 31141 MW; 307A1FE3B627D6E7 CRC64;

Query Match 9.9%; Score 101; DB 1; Length 269;
Best Local Similarity 24.4%; Pred. No. 0.017;
Matches 39; Conservative 34; Mismatches 65; Indels 22; Gaps 8;

QY 4 CDRRETFKGNKSPFKRLRGPKVKNLNPKKFSIHDHKLVLVDSNLTAVPKN--YIR 61
DB 111 CDIESD-----SFRLL-----VSSQCTTIQDINQKALSKASELALHLNRRNTS 157
QY 62 PEIFFALASSLSASAEKSPILLGVSGEFLCYCDKDKGQSHPSLQKKERLMLAAQK 121

Db 158 QOVIFSMKYYLIGDIGSOK-FHVYLCIKNNLYLSCVR-RGEK-PILQL-EQIANPFSIN 212
OY 122 ESARRPFIFYRAOYGSNNMLESAAHPGWFICTSCNCPV 161
Db 213 VEKR-FIFNKVEIINTTEFESAEPNMYISTSQMDEQPV 250

Search completed: May 3, 2003, 18:35:42
job time : 67 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2003, 18:21:35 ; Search time 89 Seconds

(without alignments)
444,506 Million cell updates/sec

Title: US-09-876-790-3

Perfect score: 1017
Sequence: 1 MSGCDRETFETGKNSFKRR.....IEFSFQPVCKAKMSPSEVSD 192

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1017	100.0	192	4	Q9UHA6	Q9UHA6 homo sapien
2	905	89.0	197	4	Q8TD05	Q8TD05 homo sapien
3	895	88.0	218	4	Q9NZH6	Q9NZH6 homo sapien
4	895	88.0	218	4	Q9HBF3	Q9HBF3 homo sapien
5	704	69.2	178	4	Q9HBF2	Q9HBF2 homo sapien
6	688	67.6	157	4	Q8TD04	Q8TD04 homo sapien
7	229	22.5	157	4	Q9UHA5	Q9UHA5 homo sapien
8	225.5	22.2	169	4	Q9NZH8	Q9NZH8 homo sapien
9	209	20.6	158	4	Q9UHA7	Q9UHA7 homo sapien
10	199	19.6	156	11	Q8R461	Q8R461 mus musculu
11	199	19.6	183	11	Q9D626	Q9D626 mus musculu
12	189.5	18.6	155	11	Q9QYX1	Q9QYX1 mus musculu
13	189.5	18.6	156	11	Q9JIG2	Q9JIG2 mus musculu
14	178.5	17.6	164	11	Q8R460	Q8R460 mus musculu
15	172.5	17.0	155	4	Q9UBH0	Q9UBH0 homo sapien
16	171.5	16.9	160	11	Q9JLA2	Q9JLA2 mus musculu

17	165.5	16.3	152	11	Q8R459	Q8R459 mus musculu
18	156.5	15.4	152	4	Q8WZ1	Q8WZ1 homo sapien
19	156	15.3	144	4	Q9BYX1	Q9BYX1 homo sapien
20	155.5	15.3	152	4	Q969H5	Q969H5 homo sapien
21	151	14.8	272	13	Q9DDF2	Q9DDF2 cyprinus ca
22	150	14.7	177	6	Q9GMD4	Q9GMD4 tursiops tr
23	149.5	14.7	159	4	Q9GMD6	Q9GMD6 homo sapien
24	149	14.7	176	6	Q9BEH0	Q9BEH0 homo sapien
25	149	14.7	267	13	Q73909	Q73909 gallus galli
26	140	13.8	272	13	Q9DDF3	Q9DDF3 cyprinus ca
27	139	13.7	176	6	Q9GKR2	Q9GKR2 canis famli
28	128	12.6	276	13	Q57398	Q57398 cyprinus ca
29	128	12.6	276	13	Q9PM18	Q9PM18 cyprinus ca
30	118.5	11.7	164	4	Q9NZH7	Q9NZH7 homo sapien
31	112.5	11.1	260	13	Q8U0G3	Q8U0G3 oncorhynch
32	112.5	11.1	260	13	Q9YGD3	Q9YGD3 oncorhynch
33	112.5	11.1	267	6	Q29082	Q29082 sus scrofa
34	111.5	11.0	247	13	Q8QGW0	Q8QGW0 paralicthy
35	107	10.5	72	6	Q77771	Q77771 equus caball
36	107	10.5	254	13	Q9PT12	Q9PT12 oncorhynch
37	107	10.5	283	13	Q9PVZ5	Q9PVZ5 xenopus lae
38	104	10.2	599	11	Q91WP7	Q91WP7 mus musculu
39	103	10.1	266	6	Q8WNR2	Q8WNR2 delphinapte
40	101	9.9	253	13	Q90W32	Q90W32 sparus aura
41	101	9.9	261	13	Q90W84	Q90W84 dicentrarch
42	99	9.7	266	6	Q9TTK1	Q9TTK1 tursiops tr
43	96	9.4	267	11	Q91ZL5	Q91ZL5 sigmodon hi
44	89.5	8.8	153	4	Q43645	Q43645 homo sapien
45	87	8.6	1064	4	Q9H7R7	Q9H7R7 homo sapien

ALIGNMENTS

RESULT 1
ID Q9UHA6 PRELIMINARY: PRT: 192 AA.
AC Q9UHA6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE FILI zeta.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20092888; PubMed=10625660;
RA Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garika K.F.,
RT Sims J.E.;
RT *Four New Members Expand the IL-1 Superfamily.*;
RL J. Biol. Chem. 275:1169-1175(2000).
DR EMBL: AF201832; AAF25212.1; -.
DR HSSP: P18510; 1ILR.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; 1IL; 1.
DR ProDom: PD002536; Interleukin_1; 1.
DR SMART: SM00125; 1IL; 1.
DR SMART: SM00125; 1IL; 1.
SQ SEQUENCE 192 AA; 21543 MW; 4AF584C81802FE612 CRC64;

Query Match 100.0%; Score 1017; DB 4; Length 192;
Best Local Similarity 100.0%; Pred. NO. 2.9e-96;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGCDRETFETGKNSFKRR...LPKFSIHQDHKVLVLDGNTLAVPDKNYI 60
DB 1 MSGCDRETFETGKNSFKRR...LPKFSIHQDHKVLVLDGNTLAVPDKNYI 60
QY 61 REITFFALASSLSAEGSPILIGVSKGECCLYCDKDKGSHPSLQKKKELKMLAAQ 120
DB 61 REITFFALASSLSAEGSPILIGVSKGECCLYCDKDKGSHPSLQKKKELKMLAAQ 120

```

QY 121 KESARRPFYRAQVGSNMLESAAHPGFIOTSCNCPNPGVTDKFNKRHIIEFQPV 180
DB 121 KESARRPFYRAQVGSNMLESAAHPGFIOTSCNCPNPGVTDKFNKRHIIEFQPV 180
QY 181 CAEMSPSEVSD 192
DB 181 CAEMSPSEVSD 192

RESULT 2
Q8TD05 PRELIMINARY: PRT: 197 AA.
AC Q8TD05;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE IL-1F7d.
GN IL1F7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Taylor S.L., Renshaw B.R., Garka K.E., Smith D.E., Sims J.E.;
RT "Genomic Organization of the IL-1 Locus.";
RL Genomics 0:0-0(2002).
DR EMBL: AY071840; AAL67151.1; -
SQ SEQUENCE 197 AA; 21950 MW; 55BEA654008B67A CRC64;

Query Match 89.0%; Score 905; DB 4; Length 197;
Best Local Similarity 99.4%; Pred. No. 9,1e-85;
Matches 171; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 LGGPKYKNNPKKFSIHODHKVLYLDSGNLIAPDKNTYRPEIFALASSLSASAERG 80
DB 26 LGGPKYKNNPKKFSIHODHKVLYLDSGNLIAPDKNTYRPEIFALASSLSASAERG 85
QY 81 SPILGVSKEGFCYCDKDGKSHPSLOLKKELKMLAOKESARRPFYRAQVGSNM 140
DB 86 SPILGVSKEGFCYCDKDGKSHPSLOLKKELKMLAOKESARRPFYRAQVGSNM 145
QY 141 LESAAHPGFIOTSCNCPNPGVTDKFNKRHIIEFQPVCAEMSPSEVSD 192
DB 146 LESAAHPGFIOTSCNCPNPGVTDKFNKRHIIEFQPVCAEMSPSEVSD 197

RESULT 3
Q9NZH6 PRELIMINARY: PRT: 218 AA.
AC Q9NZH6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Interleukin-1 homolog 4 (IL-1x protein) (Interleukin-1-related protein long isoform a).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=FETAL LUNG, FETAL TESTIS, FETAL B-CELL, AND FETAL COLON;
RX MEDLINE=20209405; PubMed=10744718;
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA Young P.R.;
RT "Identification and initial characterization of four novel members of the interleukin-1 family.";
RL J. Biol. Chem. 275:10308-10314(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON CARCINOMA;

```

```

RA Manoj P.P., Mantovani A., Muzio M.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Pan G., Rissler P., Mao W., Baldwin D.T., Zhong A.W., Yansura D.,
RA Lewis L., Eigenbrodt C., Henzel W.J., Vandlen R., Filvaroff E.;
RT "IL-1H, an interleukin-1-related protein that binds IL-18 receptor/IL-1Rr.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF200496; AAF69252.1; -
DR EMBL: AF167368; AAG29344.1; -
DR EMBL: AF251118; AAG14420.1; -
DR HSSP: P18510; 1ILR.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR ProDom: PD002536; Interleukin_1; 1.
DR SMART: SM00125; IL1; 1.
SQ SEQUENCE 218 AA; 24126 MW; 96E089310D2CEA68 CRC64;

```

```

Query Match 88.0%; Score 895; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 1,1e-83;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 PKYKNNPKKFSIHODHKVLYLDSGNLIAPDKNTYRPEIFALASSLSASAERGSP1 83
DB 50 PKYKNNPKKFSIHODHKVLYLDSGNLIAPDKNTYRPEIFALASSLSASAERGSP1 109
QY 84 LLSGSKGEFCLYCDKDGKSHPSLOLKKELKMLAOKESARRPFYRAQVGSNM 143
DB 110 LLSGSKGEFCLYCDKDGKSHPSLOLKKELKMLAOKESARRPFYRAQVGSNM 169
QY 144 AAHPGFIOTSCNCPNPGVTDKFNKRHIIEFQPVCAEMSPSEVSD 192
DB 170 AAHPGFIOTSCNCPNPGVTDKFNKRHIIEFQPVCAEMSPSEVSD 218

RESULT 4
Q9HBF3 PRELIMINARY: PRT: 218 AA.
AC Q9HBF3;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Interleukin-1-related protein long isoform (Hypothetical 24.1 kDa protein).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=11066552; PubMed=11145836;
RA Pan G., Rissler P., Mao W., Baldwin D.T., Zhong A.W., Filvaroff E.,
RA Yansura D., Lewis L., Eigenbrodt C., Henzel W.J., Vandlen R.,
RT "IL-1H, an interleukin-1-related protein that binds IL-18 receptor/IL-1Rr.";
RL Cytochrome 13:1-7(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF251119; AAG14421.1; -
DR HSSP: BC020637; AAH20637.1; -
DR HSSP: P18510; 1ILR.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR ProDom: PD002536; Interleukin_1; 1.
DR SMART: SM00125; IL1; 1.
KW Hypothetical protein.
SQ SEQUENCE 218 AA; 24138 MW; 76E09C35093DEA63 CRC64;

```

Query Match 88.0%; Score 895; DB 4; Length 218;

8HZN60

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. Q9NZH8

```

ID 09NZH8 PRELIMINARY; PRT; 169 AA.
AC 09NZH8;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE Interleukin-1 homolog 1 (Interleukin-1 epsilon).
GN ILE
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE FROM N.A.
RX MEDLINE=20209405; PubMed=10744718;
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA Young P.R.;
RT "Identification and initial characterization of four novel members of
RT the interleukin-1 family."
RL J. Biol. Chem. 275:10308-10314(2000).
RP SEQUENCE FROM N.A.
RC TISSUE=AIRWAY EPITHELIAL CELLS INDUCED WITH TNF ALPHA, AND IPN;
RA Debets R., Timans J., Zurawski S., Bazan J.F., Kastelein R.A.;
RT "Novel IL-1 family member IL-1e responds through the orphan IL-1R-
RT related protein 2: response is antagonized by IL-1d."
RL Submitted (NOV-1999) to the EMBL/Genbank/DBD databases.
DR EMBL; AF200492; AAF69248.1; -
DR HSSP; P18510; 11LR.
DR HSSP; P18510; 11TN.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR ProDom: PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 169 AA; 18721 MW; F00A9243706F4154 CRC64;

Query Match
Best Local Similarity 38.3%; Score 225.5; DB 4; Length 169;
Matches 51; Conservative 26; Mismatches 51; Indels 5; Gaps 4;

QY 35 SHDQDHKVLVDSGNLAVDPKNYIRPEIFALASLSASAE-KGSPILLGSGKERC 93
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 26 TINDLNOQVTLQGNLVAVPRSDSVTPVAVITCKYEALQEGGDPYVIGLNPENC 85
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 94 LYCDKKGSHPSLOKKEKKMLAOKESARRPFTFYRAQVGSNNMLESAAHPGWFCT 153
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 86 LTCEKGEQ--PTLQKEKIDMLYGPPEV-KPFLFYRAKGTSTLESVAFPDMFTAS 142
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 154 SCNCNEPVGVTDK 166
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 143 S-KRQDPILTSE 154
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
Q9UHA7 PRELIMINARY; PRT; 158 AA.
AC Q9UHA7;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE FTL1 epsilon.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE FROM N.A.
RX MEDLINE=20092888; PubMed=10625660;
RA Smith D.E., Renshaw B.R., Ketchum R.R., Kudin M., Garika K.E.,
RA Sims J.E.;
RT "Four New Members Expand the IL-1 Superfamily."
RL J. Biol. Chem. 275:1169-1175(2000).
EMBL; AF201831; AAF25211.1; -

```

```

DR HSSP; P18510; 11LR.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR ProDom: PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 158 AA; 17684 MW; 469AC84306B0E280 CRC64;

Query Match
Best Local Similarity 36.7%; Score 209; DB 4; Length 158;
Matches 54; Conservative 26; Mismatches 61; Indels 6; Gaps 4;

QY 31 PKKFSIHDDHKVLDGSLAVDPKNYIRPEIFALAS--SLSSAEEKSPILLGVS 88
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 10 PQGGSIODINHRVWVLOQTLIAVPRKDRMSR-VTIALISCRHVETLEKDRGNPVLGLN 68
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 89 KGEFLCYCDKDGSHPSLOKKEKKMLAOKESARRPFTFYRAQVGSNNMLESAAHPG 148
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 69 GINCLCMARKYGDQ--PTLQKEKIDMLYGPPEV-KSFLFYHSGSGRSTFESVAFPG 125
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 149 WFICTSCNCNEPVGVTDKFNKRKHIEF 175
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 126 WFIAVSSGGCPILLITQELGKANTTDF 152
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
Q8R461 PRELIMINARY; PRT; 156 AA.
AC Q8R461;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE IL-1F8.
GN IL1F8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RA STRAIN=SWISS WEBSTER/NIH;
RA Taylor S.L., Renshaw B.R., Garika K.E., Smith D.E., Sims J.E.;
RL "Genomic Organization of the IL-1 Locus."
DR EMBL; AY071842; AAL67152.1; -
SQ SEQUENCE 156 AA; 17775 MW; 868FBE63BF243BBF CRC64;

Query Match
Best Local Similarity 19.6%; Score 199; DB 11; Length 156;
Matches 42; Conservative 27; Mismatches 53; Indels 4; Gaps 3;

QY 30 NPKKFSIHDDHKVLDGSLAVDPKNYIRPEIFALAS--SLSSAEEKSPILLGVS 88
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 7 SPRNRYRHDSQOMVWVLTGNTLFAVPASNNVKKPILSLICRDLPEQDVAKKGLVFLGIR 66
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 89 KGEFLCYCDKDGSHPSLOKKEKKMLAOKESARRPFTFYRAQVGSNNMLESAAHPG 148
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 67 NRNICFCCEWVEGK--PTLQKEKIDMLYKERR-AQKAPLFYHGIEGTSVQSVLYTPG 123
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 149 WFICTS 154
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 124 WFIAVS 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
Q9D6Z6 PRELIMINARY; PRT; 183 AA.
AC Q9D6Z6;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE 2310043N20R4K protein.
GN 2310043N20R4K
OS Mus musculus (Mouse).

```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBL_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TONGUE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK009787; BAB26505.1; -
DR HSSP; P01584; 1H1B.
DR MGD; MGI:1916927; 2310043N20R1k.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; UNKNOMN_1.
SQ SEQUENCE 183 AA; 20878 MW; A3ACE339FB96F02E CRC64;

Query Match 19.6%; Score 199; DB 11; Length 183;
Best Local Similarity 33.3%; Pred. No. 2e-12;
Matches 42; Conservative 27; Mismatches 53; Indels 4; Gaps 3;

OY 30 NPKKFSIHDDQKVLVDSCNLIATVPDKNYIRPEIFALASLSASAEGKSPILGYSGE 88
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 34 SPRNRVHDSQGMVWVLTNGNLTAVPASNNKPVLLSLACRDFEQVKKGNLVFLGK 93
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 89 KGEFLYCDKDGKQSHPSIQLKKEKIMKLAQKESARPPFIYRAQVSWNMLESAHPG 148
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 94 NNNLCFCCCEMGRK--PTLQLEKVEDIMNLYKERK-AQKAFLEHGIESTSVFQSVLPYG 150
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 149 WFICTS 154
   ||| ||
DB 151 WFICTS 156

RESULT 12
O90Y11 PRELIMINARY; PRT; 155 AA.
AC O90Y11:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE IL-11 protein (interleukin-1 homolog 3).
GN IL1F5 OR IL1H1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBL_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Barton J.L., Nicklin M.J.H.;
RT "IL-11: A Novel Member of the Interleukin-1 Gene Family is Expressed in Trophectoderm and Macrophages.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

```

```

RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209405; PubMed=10744718;
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA Young P.R.;
RT "Identification and initial characterization of four novel members of the interleukin-1 family.";
RL J. Biol. Chem. 275:10308-10314(2000).
DR EMBL; AJ250429; CAB59831.1; -
DR EMBL; AF200495; AAF69251.1; -
DR HSSP; P18510; 1ILR.
DR MGD; MGI:1859325; IL1F5.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; UNKNOMN_1.
SQ SEQUENCE 155 AA; 17004 MW; A4B1770F2E12533A CRC64;

Query Match 18.6%; Score 189.5; DB 11; Length 155;
Best Local Similarity 37.3%; Pred. No. 1.5e-11;
Matches 50; Conservative 23; Mismatches 50; Indels 11; Gaps 5;

OY 34 FSIHDDQKVLVDSCNLIATVPDKNYIRPEIFALASLSASAEGKSPILGYSGE 91
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 9 FRKMSALKVLILHNNQLLAGLHAERKIVGCEISVPPNALLDSL--SPVLGVGGG 65
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 92 FCLYCDKDGKQSHPSIQLKKEKIMKLAQKESARPPFIYRAQVSWNMLESAHPG 150
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 66 QCSICSGTEKG--PIKLEPVNIMELYLAKES--KSFTEYRDMGLTSSFAAYPGW 120
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 151 ICTSCNCEPVGVT 164
   : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 121 LCTSPEDQPPVRL 134

RESULT 13
O90Y12 PRELIMINARY; PRT; 156 AA.
AC O90Y12:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Interleukin-1 delta (Interleukin 1 receptor antagonist homolog 1).
GN IL1F5 OR IL1H1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBL_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Debets R., Timans J.C., Zurawski S., Sana T.R., Bazan F.,
RA Kastelein R.A.;
RT "Novel IL-1 ligands IL-1d and IL-1e use IL-1R related protein 2.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

```

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaertis P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shidara Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsunk S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection,"
 RL Nature 409:685-690(2001).
 DR EMBL: AF230378; AAF91275.1; -
 DR EMBL: AK009741; BAB26471.1; -
 DR EMBL: AK008977; BAB26002.1; -
 DR HSSP: P18510; IILR.
 DR MGD: MG1:1859325; I115.
 DR InterPro: IPR000975; Interleukin_1.
 DR Pfam: PF00340; IL1; 1.
 DR ProDom: PD002536; Interleukin_1; 1.
 DR SMART: SM00125; IL1; 1.
 DR PROSITE: PS00253; INTERLEUKIN_1; 1.
 SO SEQUENCE 156 AA; 17136 MW; A4D1EE2P93CF77A7 CRC64;

Query Match 18.6%; Score 189.5; DB 11; Length 156;
 Best Local Similarity 37.3%; Pred. No. 1.5e-11;
 Matches 50; Conservative 23; Mismatches 50; Indels 11; Gaps 5;

Qy 34 FSIHDOHKVLYLDSGNLIA--VPDKYIRPEIFALASSASAKSGSPILLGVSK 91
 Db 10 FRMDSAKLYLHNNOLLAGLAEKVIKGEISVVPNALDAS--SPVLLGVQGS 66
 Qy 92 FCLVCDKRGQSHPSLOLTKKELMLKLT--AAQKESARPFIRYRAQVSWNNLESAAHGMF 150
 Db 67 QCLSGITKGG--PILKLEPVNIMELYLAKES--KSTFYRRDMGLTSPESAAIPGMF 121

Qy 151 ICTSCNENPEYGV 164
 Db 122 LCTSPEDAQPVRLT 135

RESULT 14
 Q8R460 PRELIMINARY; PRT; 164 AA.

AC Q8R460;
 DT 01-JUN-2002 (TREMblrel. 21, Created)
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 GN IL1F9.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=SWISS WEBSTER/NIH;
 RA Taylor S.L., Renshaw B.R., Garika K.E., Smith D.E., Sims J.E.;
 RT "Genomic Organization of the IL-1 Locus,"
 RL EMBL: AY071943; AAL67153.1; -
 SO SEQUENCE 164 AA; 18733 MW; A7338D475DEADBE CRC64;

Query Match 17.6%; Score 178.5; DB 11; Length 164;
 Best Local Similarity 29.9%; Pred. No. 2.2e-10;
 Matches 49; Conservative 29; Mismatches 77; Indels 9; Gaps 5;

Qy 14 KNSRRKRLRGPKVKNLPKFSIHDOHKVLYLDSGNLIAVPDKYIRPEIFALASSL- 72
 Db 4 KHPSTHLSGRE---TPDGEVFDLDQVWIRNQLVYVPSRSHVTPTVSTILPCCKYP 59
 Qy 73 SSAAEKSGPILLGVSGEPCLVCDKRGQSHPSLOLTKKELMLKLAQKESARPFIRY 132
 Db 60 ESLDQDKIALYILGIQNPDKCLFEKFNWG--HPTLLKEKILDLVHNEE-PKRPPLFTH 116
 Qy 133 AQVGSWMNLESAAHGMFICTSCNENPEYGVTDKFFENRKIEPS 176

Db 117 TRTGSTSPESVAFPGHYINSSKTGN-PILFTSKGGEYYNINFN 159

RESULT 15

ID Q9UBH0 PRELIMINARY; PRT; 155 AA.

AC Q9UBH0;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE F111 delta (interleukin-1 like protein 1) (interleukin-1 receptor
 DE antagonist homolog 1) (interleukin 1, delta).
 GN IL1H1 OR IL1L1.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=20092868; PubMed=10625660;
 RA Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garika K.E.,
 RA Sims J.E.;
 RT "Four New Members Expand the IL-1 Superfamily,"
 RL J. Biol. Chem. 275:1169-1175(2000).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=99443727; PubMed=10512743;
 RA Mulero J.J., Pace A.M., Nelken S.T., Loeb D.B., Correa T.R.,
 RA Dumanac R., Ford J.E.;
 RT "IL1H1: A Novel Interleukin-1 Receptor Antagonist Gene,"
 RL Biochem. Biophys. Res. Commun. 263:702-706(1999).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Barton J.L., di Giovine F.S., Symons J.A., Nicklin M.J.H.;
 RT "A tissue specific interleukin-1 receptor antagonist homolog from the
 RT IL1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18ra activities,"
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

RA Barton J.L., Herbst R., Bosasio D., Nicklin M.J.H.;
 RT "A tissue specific interleukin-1 receptor antagonist homolog from the
 RT IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18ra activities,"
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

RA MEDLINE=2032477; PubMed=10866108;
 RA Mulero J.J., Nelken S.T., Ford J.E.;
 RT "Organization of the Human Interleukin-1 Receptor Antagonist Gene
 RT IL1H1,"
 RL Immunogenetics 51:425-428(2000).

RA Debelts R., Timans J.C., Zurawski S., Sana T.R., Bazan F.,
 RA Kastelein R.A.;
 RT "Novel IL-1 ligands IL-1d and IL-1e use IL-1R related protein 2,"
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

RA SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Strauberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF201830; AAF25210.1; -
 DR EMBL: AF186094; AAF02757.1; -
 DR EMBL: AJ242737; CAB59822.1; -
 DR EMBL: AJ242738; CAB59823.1; -
 DR EMBL: AJ271338; CAB67704.1; -
 DR EMBL: AF216693; AAF76981.1; -
 DR EMBL: AF230377; AAF91274.1; -
 DR EMBL: BC024747; AAR24747.1; -
 DR HSSP: P18510; IILR.
 DR InterPro: IPR000975; Interleukin_1.
 DR Pfam: PF00340; IL1; 1.

DR PRODOM; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 155 AA; 16962 MW; B96DB5EFA2612E25 CRC64;

Query Match	17.0%;	Score 172.5;	DB 4;	Length 155;
Best Local Similarity	33.6%;	Pred. No. 8.4e-10;		
Matches 51; Conservative	17;	Mismatches 47;	Indels 37;	Gaps 6;

```

QY      34 FSIHQDHKAVYLVDSGNLAVPDKNYIRPELFFALASSLSASAKNG----- 80
Db      9 FRMDSAIKVYLHNOL-----LAGGLAGKYIKKEELSYVPMRWLDA 52
QY      81 --SPILGVSKEGFCYCDKDGKSHPSLOKREKMKL-AAOKESARPPFIYRAQVS 137
Db      53 SLSPVILIGVGGGSOCLC--GVGO-EPTLTLEPVNIMELYIGAKES--KSFTEYRDMGL 107
QY      138 WNMLESAAHPGMPFICTSCNCENPAGVINDKFEEN 169
Db      108 TSSESAAYIPGMPFICTYVPEADQVRLTQLPEEN 139

```

Search completed: May 3, 2003, 18:37:26
Job time : 92 secs

